

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:09:54 ; Search time 95.5625 Seconds
(without alignments)
50.576 Million cell updates/sec

Title: US-10-632-706-198
Perfect score: 59
Sequence: 1 WGGCTVTVSS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	11	2	AAR85166 Human ONS
2	59	100.0	11	2	AAR97333 Humanised
3	59	100.0	11	4	AAU07452 Synthetic
4	59	100.0	11	5	AAE28561 scFv anti
5	59	100.0	11	5	AAU70517 Mouse hea
6	59	100.0	11	5	AAU70501 Mouse hea
7	59	100.0	11	5	AAU70485 Mouse hea
8	59	100.0	11	5	AAU70477 Mouse hea
9	59	100.0	11	6	ABO10719 Deimnitis
10	59	100.0	11	6	ABR44663 Murine J4
11	59	100.0	11	7	ABO33904 Anti-GPI-
12	59	100.0	11	7	ADG75671 Peptide o
13	59	100.0	11	8	ADH17960 Human mod
14	59	100.0	11	8	ADH18011 Human mod
15	59	100.0	11	8	ADG90791 Artificialia
16	59	100.0	11	8	ADR12645 Mammalian
17	59	100.0	11	8	ADR38796 Mouse hea
18	59	100.0	11	8	ADR38793 Mouse hea
19	59	100.0	11	8	ADR38802 Mouse hea
20	59	100.0	11	8	ADR38799 Mouse hea
21	59	100.0	11	8	ADU38427 Mouse ant
22	59	100.0	11	8	ADU67919 Mouse ant
23	59	100.0	11	9	ADW07403 Heavy cha
24	59	100.0	11	9	ADW07419 Heavy cha

25	59	100.0	11	9	ADM07407 Heavy cha
26	59	100.0	11	9	ADM07423 Heavy cha
27	59	100.0	11	9	ADM07427 Heavy cha
28	59	100.0	11	9	ADM07435 Heavy cha
29	59	100.0	11	9	ADM07439 Heavy cha
30	59	100.0	11	9	ADM07411 Heavy cha
31	59	100.0	11	9	ADM07443 Heavy cha
32	59	100.0	11	9	ADM07451 Heavy cha
33	59	100.0	11	9	ADM07415 Heavy cha
34	59	100.0	11	9	ADM07447 Heavy cha
35	59	100.0	11	9	ADM07431 Heavy cha
36	59	100.0	11	9	ADY31581 Human ant
37	59	100.0	11	9	ADZ35850 Anti-glic
38	59	100.0	11	9	ADZ83544 CD3 const
39	59	100.0	11	9	ADZ83542 CD3 const
40	59	100.0	11	9	ADZ83545 CD3 const
41	59	100.0	11	9	ADZ83543 CD3 const
42	59	100.0	11	9	AEA21481 Human ant
43	59	100.0	11	9	AEA21445 Human ant
44	59	100.0	11	9	AEA45691 Apolipop
45	59	100.0	11	9	AEA44171 Anti-TP0

ALIGNMENTS

RESULT 1
AAR85166
ID AAR85166 standard; protein; 11 AA.
AC AAR85166;
XX 18-JAN-1996 (first entry)
DT
XX
XX Human ONS-M21 antibody heavy variable region FR 4.
DE
XX Human; ONS-M21 antibody; heavy variable region; chimeric protein;
KW framework region; FR 4; medulloblastoma; brain tumour; treatment;
KW diagnosis.
XX
XX Homo sapiens.
OS
XX
XX MO9514041-A1.
PN
XX 26-MAY-1995.
PD
XX 19-OCT-1994; 94WO-JP001763.
PE
XX 19-NOV-1993; 93JP-00291078.
PR
XX (CHUS) CHUGAI SEIYAKU KK.
PA
XX Ohtomo T, Sato K, Tsuchiya M;
PI WPI; 1995-200347/26.
XX
XX Reconstituted antibody against human medullo:blastoma cells - contains
PT high proportion of human antibody origin and has low antigenicity.
XX
XX Claim 18; Page 102; 120pp; Japanese.
PS
XX AAR85163-R85166 are human antibody ONS-M21 heavy variable region
CC framework regions (FRs). They were used in the construction of a
CC human/murine chimeric antibody, reactive with human medullo:blastoma (a
CC brain tumour) cells. The chimeric antibody can be used in the diagnosis
CC and treatment of this disease
XX
XX Sequence 11 AA;
SQ
Query Match 100.0%; Score 59; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
 |||||
 DB 1 WGGGTTTVSS 11

RESULT 2

AAR97333

ID AAR97333 standard; peptide; 11 AA.

AC AAR97333;

DT 15-OCT-1996 (first entry)

DE Humanised monoclonal antibody heavy chain framework region.

XX Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
 KW complementary determining region; anti-carcinoma/embryonic antigen; CEA;
 XX diagnosis; imaging; therapy; immune response.

OS Homo sapiens.

PN WO9611013-A1.

PD 18-APR-1996.

PF 28-SEP-1995; 95WO-US011964.

PR 05-OCT-1994; 94US-00318157.

PA (IMMU-) IMMUNOMEDICS INC.

PI Hansen HJ, Armour KL;

DR WPI; 1996-209653/21.

PT New humanised anti-CEA monoclonal antibody - having engrafted murine
 CDR, used for diagnosis, imaging and therapy of CEA-producing cancers.

PS Claim 7, Page 40; 62pp; English.

CC New humanised monoclonal antibodies (MAbs) comprising the complementary
 CC determining regions (CDRs) of a parental murine class III anti-
 CC carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
 CC human, retain the anti-CEA binding specificity of the parental murine MAb
 CC but are less immunogenic in a human subject than the parental MAb. The
 CC humanised antibodies can be used in diagnosis, imaging and therapy of CEA
 CC -producing cancers and patients receiving the humanised antibodies and
 CC conjugates show improved therapeutic results, decreased immune responses
 CC and decreased immune-mediated adverse effects compared to the parent
 CC antibody. This sequence corresponds to the fourth framework region of the
 CC heavy chain of the humanised MAb. See AAR97333-97333

SQ Sequence 11 AA;

Query Match 100.0%; Score 59; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
 |||||
 DB 1 WGGGTTTVSS 11

RESULT 3

AAU07452

ID AAU07452 standard; peptide; 11 AA.

AC AAU07452;

DT 24-OCT-2001 (first entry)

DE Synthetic peptide H-FR4-F8.

XX H-FR4-F8; antimicrobial; antiviral; cytostatic; immunomodulatory;
 KW antibody; gene therapy; HIV; human immunodeficiency virus; tumour;
 KW metabolic disorder; immune disorder; auto-immune disorder.

OS Synthetic.

PN WO200149713-A2.

PD 12-JUL-2001.

PE 29-DEC-2000; 2000WO-IT000554.

PR 30-DEC-1999; 99IT-RM000803.

PA (CNSN) ENEA ENTE NUOVE TECNOLOGIE ENERGIA.

XX (CONS-) SOC CONSORTILE METAPONTUM AGRIBIOS SRL.
 PI Benvenuto E, Franconi R, Desiderio A, Taviadoraki P;

XX WPI; 2001-502555/55.

DR N-PSDB; AAS11874.

PT Peptides which are able to confer stability and solubility to an antibody
 PT comprising these peptides, useful for treating pathologies (e.g. tumor)
 PT associated with accumulation of a molecule inside or outside a human, or
 PT animal cell.

PS Claim 1; Page 57; 109pp; English.

CC The invention relates to peptides which are able to confer stability and
 CC solubility to an antibody comprising these peptides. The peptides are
 CC especially H-FR1, H-FR2, HF-R3, HFR4, L-FR1, L-FR2, L-FR3 or L-FR4
 CC present within a variable region of an antibody which makes the antibody
 CC soluble and stable in cytoplasm. Peptides having the sequences of HFRI to
 CC H-FR4 are present within the variable region of the heavy chain of an
 CC antibody, covalently linked to the H-CDR1, H-CDR2, H-CDR3 in the order (H
 CC -FR1)-(H-CDR1)-(H-FR2)-(H-CDR2)-(H-CDR3)-(H-CDR4) and peptides
 CC having the sequences of L-FR1 to L-FR4 are present within the variable
 CC region of the light chain of an antibody, covalently linked to the L-
 CC CDR1, L-CDR2, L-CDR3 in the order (L-FR1)-(L-CDR1)-(L-FR2)-(L-CDR2)-
 CC (L-FR3)-(L-CDR3)-(L-CDR4). The antibodies and polynucleotides are useful
 CC (e.g. by gene therapy) for the manufacture of a medicament for the
 CC treatment of pathologies associated with accumulation of a molecule
 CC inside or outside a human, animal cell or plant cell. The pathologies are
 CC infectious (e.g. viral infections such as HIV, human immunodeficiency
 CC virus, infections), tumour, metabolic and immune (especially auto-immune)
 CC pathologies. The present sequence represents the peptide H-FR4-F8 (also
 CC known as H-FR4)

SQ Sequence 11 AA;

Query Match 100.0%; Score 59; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
 |||||
 DB 1 WGGGTTTVSS 11

RESULT 4

AAE28561

ID AAE28561 standard; peptide; 11 AA.

AC AAE28561;

DT 27-DEC-2002 (first entry)

DE scFv antibody heavy chain framework region 4 from S18 clone.

XX Human; sugar-nucleic acid interaction; single chain human antibody; scFv;
 KW L-peptide binder; D-nucleic acid binder; sugar-protein interaction; FR4;

KW frame work region 4.
 XX Homo sapiens.
 XX
 XX WO200267860-A2.
 XX
 XX 06-SEP-2002.
 XX
 XX 22-FEB-2002; 2002MO-US005193.
 XX
 XX 22-FEB-2001; 2001US-0271377P.
 XX
 XX (SCRI) SCRIPPS RES INST.
 XX
 XX Wong C;
 XX
 XX WPI; 2002-691633/74.
 XX
 XX Selecting L-peptide or D-nucleic acid binders that binds to enantiomers
 PT of naturally occurring carbohydrate, comprises providing enantiomers of
 PT naturally occurring carbohydrate, and screening library against
 PT enantiomers.
 XX
 XX Disclosure; Fig 6B; 46pp; English.
 XX
 XX The present invention relates to a novel method of selecting L-peptide or
 CC D-nucleic acid binders that bind to enantiomers of naturally occurring
 CC sugar or carbohydrate. The method involves providing enantiomers of
 CC naturally occurring sugar or carbohydrate employable for screening the
 CC library and then screening the library against the enantiomers for
 CC identifying a L-peptide binder or D-nucleic acid binder having binding
 CC activity with respect to enantiomers. The method is useful for selecting
 CC L-peptide binder or D-nucleic acid binder that binds to enantiomer of
 CC naturally occurring sugar or carbohydrate. It is useful for selecting L-
 CC peptide binders and/or L-nucleic acid binders that are resistant to
 CC enzymatic degradation due to their non-naturally occurring chirality, for
 CC blocking or activating the biological function of the naturally occurring
 CC sugar or carbohydrate to which they are targeted. The naturally occurring
 CC sugar and carbohydrates include bacterial or viral cell surface sugars
 CC or carbohydrates, heparin sulphates involved in viral entry, thrombosin
 CC and angiotensin. The method is useful for identifying D-peptides, for
 CC studying sugar-protein and sugar-nucleic acid interaction and for
 CC designing high-affinity and hydrolase resistant molecules as artificial
 CC receptors capable of binding natural carbohydrates. The immobilised
 CC enantiomers are useful for screening phage expressing a peptide library
 CC on the coat proteins to identify specific clones that bind to an
 CC immobilised enantiomer. The present sequence is single chain human
 CC antibody (scfv) heavy chain frame work region 4 (PR4) from S18 clone.
 CC This sequence is used to illustrate the method of the invention
 XX
 XX Sequence 11 AA;
 XX
 XX Query Match 100.0%; Score 59; DB 5; Length 11;
 XX Best Local Similarity 100.0%; Pred. No. 0.011;
 XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 WGGGTTTVSS 11
 XX |||||
 XX 1 WGGGTTTVSS 11
 XX
 XX RESULT 5
 XX AAU70517
 XX AAU70517 standard; peptide; 11 AA.
 XX
 XX AAU70517;
 XX
 XX 14-FEB-2002 (first entry)
 XX
 XX Mouse heavy chain immunoglobulin framework region 4 #11.
 XX
 XX Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
 KW complementarity determining region; framework region; IgBP;
 KW

KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
 XX IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
 XX
 XX Mus musculus.
 XX
 XX WO200183806-A1.
 XX
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001MO-US014349.
 XX
 XX 02-MAY-2000; 2000US-00563222.
 XX
 XX (EPIC-) EPICYTE PHARM INC.
 XX
 XX Hiatt AC, Hein MB;
 XX
 XX WPI; 2002-055482/07.
 XX
 XX Preparing immunoglobulin binding protein array in plant cells by
 PT transforming the cells with different polynucleotides encoding binding
 PT protein polypeptides specific to ligand, selecting plant cells for
 PT preparing array.
 XX
 XX Disclosure; Fig 1B; 129pp; English.
 XX
 XX The invention relates to transforming a population of cells (e.g. plant
 CC cells), comprising using a library of two different polynucleotides
 CC encoding different immunoglobulin binding protein (IgBP) polypeptides
 CC that specifically bind to a ligand or form one or more disulphide bonds
 CC with polypeptides in transfected cells, to generate an IgBP that binds to
 CC a ligand, and transformed plant cells are selected, and preparing an IgBP
 CC array in plant cells. At least one peptide sequence has at least 75%
 CC sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
 CC IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
 CC useful for preparing an immunoglobulin binding protein array, preferably
 CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
 CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
 CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
 CC discovery of e.g. screening assays of IgBPs having desired
 CC characteristics. The present sequence is a mammalian immunoglobulin
 CC derived peptide that may be incorporated into an IgBP of the invention
 XX
 XX Sequence 11 AA;
 XX
 XX Query Match 100.0%; Score 59; DB 5; Length 11;
 XX Best Local Similarity 100.0%; Pred. No. 0.011;
 XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 WGGGTTTVSS 11
 XX |||||
 XX 1 WGGGTTTVSS 11
 XX
 XX RESULT 6
 XX AAU70501
 XX AAU70501 standard; peptide; 11 AA.
 XX
 XX AAU70501;
 XX
 XX 14-FEB-2002 (first entry)
 XX
 XX Mouse heavy chain immunoglobulin framework region 4 #7.
 XX
 XX Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
 KW complementarity determining region; framework region; IgBP;
 KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
 KW IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
 XX
 XX Mus musculus.
 XX
 XX WO200183806-A1.
 XX

PD 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US014349.
XX
XX 02-MAY-2000; 2000US-00563222.
PR
XX (EPIC-) EPICYTE PHARM INC.
XX
XX Hiact AC, Hein MB;
XX
XX WPI; 2002-055482/07.
DR
XX
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PT transforming the cells with different polynucleotides encoding binding
PT protein polypeptides specific to ligand, selecting plant cells for
PT preparing array.
XX
XX
PS Disclosure; Fig 1B; 129pp; English.
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XX cells), comprising using a library of two different polynucleotides
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XX with polypeptides in transfected cells, to generate an IgBP that binds to
XX a ligand, and transformed plant cells are selected, and preparing an IgBP
XX array in plant cells. At least one peptide sequence has at least 75%
XX sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
XX IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
XX useful for preparing an immunoglobulin binding protein array, preferably
XX heavy chain binding protein (CHBP) array in eukaryotic cells especially
XX plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
XX cells (e.g. insect cells or mammalian cells). The CHBP is useful for
XX discovery of e.g. screening assays of IgBPs having desired
XX characteristics. The present sequence is a mammalian immunoglobulin
XX derived peptide that may be incorporated into an IgBP of the invention
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 59; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTVSS 11
|||
DB 1 WGGGTTVTVSS 11

RESULT 7
AAU70485 standard; peptide; 11 AA.
ID AAU70485 standard; peptide; 11 AA.
XX
XX AAU70485;
AC
XX
XX 14-FEB-2002 (first entry)
DT
XX
XX Mouse heavy chain immunoglobulin framework region 4 #3.
DE
XX Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
XX complementarity determining region; framework region; IgBP;
XX transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
XX IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
KM
XX Mus musculus.
OS
XX WO200183806-A1.
PN
XX 08-NOV-2001.
PD
XX 02-MAY-2001; 2001WO-US014349.
PF
XX 02-MAY-2000; 2000US-00563222.
PR
XX (EPIC-) EPICYTE PHARM INC.
PA

XX
XX Hiact AC, Hein MB;
PI
XX WPI; 2002-055482/07.
DR
XX
XX Preparing immunoglobulin binding protein array in plant cells by
PT transforming the cells with different polynucleotides encoding binding
PT protein polypeptides specific to ligand, selecting plant cells for
PT preparing array.
XX
XX
PS Disclosure; Fig 1B; 129pp; English.
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XX The invention relates to transforming a population of cells (e.g. plant
XX cells), comprising using a library of two different polynucleotides
XX encoding different immunoglobulin binding protein (IgBP) polypeptides
XX that specifically bind to a ligand or form one or more disulphide bonds
XX with polypeptides in transfected cells, to generate an IgBP that binds to
XX a ligand, and transformed plant cells are selected, and preparing an IgBP
XX array in plant cells. At least one peptide sequence has at least 75%
XX sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
XX IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
XX useful for preparing an immunoglobulin binding protein array, preferably
XX heavy chain binding protein (CHBP) array in eukaryotic cells especially
XX plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
XX cells (e.g. insect cells or mammalian cells). The CHBP is useful for
XX discovery of e.g. screening assays of IgBPs having desired
XX characteristics. The present sequence is a mammalian immunoglobulin
XX derived peptide that may be incorporated into an IgBP of the invention
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 59; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTVSS 11
|||
DB 1 WGGGTTVTVSS 11

RESULT 8
AAU70477 standard; peptide; 11 AA.
ID AAU70477 standard; peptide; 11 AA.
XX
XX AAU70477;
AC
XX
XX 14-FEB-2002 (first entry)
DT
XX
XX Mouse heavy chain immunoglobulin framework region 4 #1.
DE
XX Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
XX complementarity determining region; framework region; IgBP;
XX transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
XX IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
KM
XX Mus musculus.
OS
XX WO200183806-A1.
PN
XX 08-NOV-2001.
PD
XX 02-MAY-2001; 2001WO-US014349.
PF
XX 02-MAY-2000; 2000US-00563222.
PR
XX (EPIC-) EPICYTE PHARM INC.
PA
XX
XX Hiact AC, Hein MB;
PI
XX WPI; 2002-055482/07.
DR
XX
PT Preparing immunoglobulin binding protein array in plant cells by
PT transforming the cells with different polynucleotides encoding binding

PT protein polypeptides specific to ligand, selecting plant cells for
PT preparing array.
XX
PS Disclosure; Fig 1B; 123pp; English.
XX
CC The invention relates to transforming a population of cells (e.g. plant
CC cells), comprising using a library of two different polynucleotides
CC encoding different immunoglobulin binding protein (IGBP) polypeptides
CC that specifically bind to a ligand or form one or more disulphide bonds
CC with polypeptides in transfected cells, to generate an IGBP that binds to
CC a ligand, and transformed plant cells are selected, and preparing an IGBP
CC array in plant cells. At least one peptide sequence has at least 75%
CC sequence identity to a framework region (FR) of a native IgbM, IgbG,
CC IgbD, IgbE, IgbY, kappa or lambda immunoglobulin molecule. The method is
CC useful for preparing an immunoglobulin binding protein array, preferably
CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
CC discovery of e.g. screening assays of IGBPs having desired
CC characteristics. The present sequence is a mammalian immunoglobulin
CC derived peptide that may be incorporated into an IGBP of the invention
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 59; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WGGGTTVTSS 11
Db 1 WGGGTTVTSS 11
RESULT 9
ABO10719
ID ABO10719 standard; peptide; 11 AA.
XX
AC ABO10719;
XX
DT 20-AUG-2003 (first entry)
XX
DE Deimmunised murine J415-4 antibody framework sequence VHFR4.
XX
KW Modified antibody; deimmunised antibody; anti-PM5A antibody;
KW prostate specific membrane antigen; immunogenic; CDR; murine;
KW complementarily determining region; J591; J415; J533; E99; mouse;
KW prostatic disorder; cancerous disorder; genitourinary inflammation;
KW prostaticis; benign enlargement; prostatic cancer; testicular cancer;
KW solid tumour; soft tissue tumour; metastatic lesion; pain; analgesic;
KW antiinflammatory; cytostatic; framework region; variable heavy chain;
KW variable light chain; VH; VL; variable region; mutant; mutain.
XX
OS Mus musculus.
OS Synthetic.
XX
PN WO200298897-A2.
XX
PD 12-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-US017068.
XX
PR 01-JUN-2001; 2001US-0295214P.
PR 20-SEP-2001; 2001US-0323585P.
PR 08-MAR-2002; 2002US-0362810P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Bander N, Carr FJ, Hamilton A;
XX
DR WPI; 2003-156839/15.
XX
PT New modified anti-prostate specific membrane antigen (PSMA)
PT immunoglobulins, useful for treating or preventing a prostatic or

PT cancerous disorder, e.g. genitourinary inflammation, prostatitis, or
PT prostatic or testicular cancer.
XX
PS Disclosure; Page 21; 254pp; English.
XX
CC The present invention relates to modified (e.g. deimmunised) antibodies
CC to prostate specific membrane antigen (PSMA). The modified anti-PSMA
CC antibodies are less immunogenic compared to the unmodified anti-PSMA
CC antibodies. The modified antibodies comprise complementarily determining
CC regions (CDRs) from a non-human antibody (e.g. murine antibody J591, J415,
CC J533 or E99), and framework sequences that are less immunogenic in humans
CC (e.g. less antigenic than the murine frameworks in which a murine CDR
CC naturally occurs). The modified antibodies bind with PM5A, preferably
CC human PM5A, with high affinity and specificity. The anti-PM5A antibodies
CC are useful for treating or preventing a prostatic or cancerous disorder,
CC e.g. genitourinary inflammation, prostatitis, benign enlargement,
CC prostatic cancer or testicular cancer, or solid tumours, soft tissue
CC tumours or metastatic lesions, and its associated pain. The present
CC sequence represents a deimmunised murine framework region
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 59; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WGGGTTVTSS 11
Db 1 WGGGTTVTSS 11
RESULT 10
ABR44663
ID ABR44663 standard; peptide; 11 AA.
XX
AC ABR44663;
XX
DT 25-JUL-2003 (first entry)
XX
DE Murine J415-4 antibody VH FR4 amino acid sequence SEQ ID NO:40.
XX
KW Mouse; murine; antibody; skin disorder; binding agent; PSMA; cytostatic;
KW prostate specific membrane antigen; antiprostatic; antiarthritic;
KW dermatological; antiinflammatory; antiallergic; vaccine; dermal disorder;
KW epidermal disorder; psoriasis; inflammatory disorder; epidermis; dermis;
KW neoplastic disorder.
XX
OS Mus musculus.
OS Synthetic.
XX
PN WO2003024388-A2.
XX
PD 27-MAR-2003.
XX
PF 30-MAY-2002; 2002WO-US017204.
XX
PR 20-SEP-2001; 2001US-0324100P.
PR 08-MAR-2002; 2002US-0362612P.
XX
PA (CORR) CORNELL RES FOUND INC.
XX
PI Bander N;
XX
DR WPI; 2003-313319/30.
XX
PT Ablating/killing aberrant prostate specific membrane antigen-expressing
PT cells for treating skin disorders, by contacting the cell with an
PT antibody that binds to the extracellular domain of prostate specific
PT membrane antigen.
XX
PS Disclosure; Page 68; 225pp; English.
XX
PT The present invention describes a method (M1) for ablating or killing an

CC excessive T cell or neutrophil activity. Accordingly, these IL-9
CC antagonists exhibit antiinflammatory, antiasthmatic and cytostatic
CC activities. This peptide sequence is a peptide from the human heavy chain
CC framework region 4, used in an exemplification of the invention.

XX
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 59; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTVTSS 11
|||
Db 1 WGGGTTVTSS 11

RESULT 13

ADH17960
ID ADH17960 standard; peptide; 11 AA.

XX AC ADH17960;

XX DT 11-MAR-2004 (first entry)

XX DE Human modified 15H12/19D12 HCA framework region 4 peptide.

XX
XX insulin-like growth factor receptor 1; IGFRI; cytosolic; osteopathic;
XX antidiabetic; antiproliferative; vasotropic; antidiarrhoeal;
XX acromegaly; bladder cancer; Wilms' tumour; ovarian; pancreatic;
XX benign prostatic hyperplasia; breast; prostate; bone; lung; colorectal;
XX cervical; synovial sarcoma; diarrhoea; carcinoma syndrome;
XX vasoactive intestinal peptide; gigantism; psoriasis; atherosclerosis;
XX smooth muscle restenosis; blood vessel; microvascular proliferation;
XX gene therapy; human; 15H12/19D12; heavy chain A; HCA; framework region.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO2003100008-A2.

XX PD 04-DEC-2003.

XX PF 22-MAY-2003; 2003WO-US016283.

XX PR 24-MAY-2002; 2002US-0383459P.

XX PR 02-JUL-2002; 2002US-0393214P.

XX PR 23-DEC-2002; 2002US-0436254P.

XX PA (SCHE) SCHERING CORP.

XX PI Wang Y, Greenberg R, Presta L, Pachter JA, Halley J, Brams P;
PI Williams D, Srinivasan M, Feingersh D;

XX DR WPI; 2004-042807/04.

XX DR N-PSDB; ADH17959.

XX PT New binding composition that specifically binds to insulin-like growth
XX factor receptor 1, useful for treating or preventing a medical condition
XX that is mediated by elevated expression or activity of IGFRI.

XX PS Disclosure; SEQ ID NO 69; 144pp; English.

XX
XX The invention relates to a novel binding composition that specifically
XX binds to insulin-like growth factor receptor 1 (IGFRI). The composition
XX of the invention demonstrates cytostatic, osteopathic,
XX antidiabetic, antiproliferative, vasotropic and antidiarrhoeal
XX activities and may be useful for preventing or treating a medical
XX condition selected from acromegaly, bladder cancer, Wilms' cancer,
XX ovarian cancer, pancreatic cancer, benign prostatic hyperplasia, breast
XX cancer, prostate cancer, bone cancer, lung cancer, colorectal cancer,
XX cervical cancer, synovial sarcoma, diarrhoea associated with carcinoid
XX syndrome, vasoactive intestinal peptide secreting tumours, gigantism,
XX psoriasis, atherosclerosis, smooth muscle restenosis of blood vessels and

CC inappropriate microvascular proliferation. The composition may also have
CC gene therapy applications. The current sequence is that of the human
CC 15H12/19D12 heavy chain A (HCA) framework region peptide of the
CC invention.

XX
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 59; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTVTSS 11
|||
Db 1 WGGGTTVTSS 11

RESULT 14

ADH18011
ID ADH18011 standard; peptide; 11 AA.

XX AC ADH18011;

XX DT 11-MAR-2004 (first entry)

XX DE Human modified 15H12/19D12 HCB framework region 4 peptide.

XX
XX insulin-like growth factor receptor 1; IGFRI; cytosolic; osteopathic;
XX antidiabetic; antiproliferative; vasotropic; antidiarrhoeal;
XX acromegaly; bladder cancer; Wilms' tumour; ovarian; pancreatic;
XX benign prostatic hyperplasia; breast; prostate; bone; lung; colorectal;
XX cervical; synovial sarcoma; diarrhoea; carcinoma syndrome;
XX vasoactive intestinal peptide; gigantism; psoriasis; atherosclerosis;
XX smooth muscle restenosis; blood vessel; microvascular proliferation;
XX gene therapy; human; 15H12/19D12; heavy chain B; HCB; framework region.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO2003100008-A2.

XX PD 04-DEC-2003.

XX PF 22-MAY-2003; 2003WO-US016283.

XX PR 24-MAY-2002; 2002US-0383459P.

XX PR 02-JUL-2002; 2002US-0393214P.

XX PR 23-DEC-2002; 2002US-0436254P.

XX PA (SCHE) SCHERING CORP.

XX PI Wang Y, Greenberg R, Presta L, Pachter JA, Halley J, Brams P;
PI Williams D, Srinivasan M, Feingersh D;

XX DR WPI; 2004-042807/04.

XX DR N-PSDB; ADH18010.

XX PT New binding composition that specifically binds to insulin-like growth
XX factor receptor 1, useful for treating or preventing a medical condition
XX that is mediated by elevated expression or activity of IGFRI.

XX PS Disclosure; SEQ ID NO 120; 144pp; English.

XX
XX The invention relates to a novel binding composition that specifically
XX binds to insulin-like growth factor receptor 1 (IGFRI). The composition
XX of the invention demonstrates cytostatic, osteopathic,
XX antidiabetic, antiproliferative, vasotropic and antidiarrhoeal
XX activities and may be useful for preventing or treating a medical
XX condition selected from acromegaly, bladder cancer, Wilms' cancer,
XX ovarian cancer, pancreatic cancer, benign prostatic hyperplasia, breast
XX cancer, prostate cancer, bone cancer, lung cancer, colorectal cancer,
XX cervical cancer, synovial sarcoma, diarrhoea associated with carcinoid
XX syndrome, vasoactive intestinal peptide secreting tumours, gigantism,
XX psoriasis, atherosclerosis, smooth muscle restenosis of blood vessels and

CC inappropriate microvascular proliferation. The composition may also have
 CC gene therapy applications. The current sequence is that of the human
 CC 15H12/19D12 heavy chain B (HCB) framework region peptide of the
 CC invention.

XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 59; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTSS 11
 |||||
 Db 1 WGGGTTVTSS 11

RESULT 15

ADQ90791
 ID ADQ90791 standard; protein; 11 AA.

AC ADQ90791;

DT 07-OCT-2004 (first entry)

DE Artificially deimmunised framework sequence #14.

XX insulin-related disorder; prostate specific membrane antigen; PSMA;

KW obesity; hyperglycaemia; hypoglycaemia; hyperinsulinaemia;

KW insulin-resistance; impaired glucose tolerance; impaired fasting glucose;

KW Type 1 diabetes mellitus; Type 2 diabetes mellitus; gestational diabetes.

OS Synthetic.

XX US2004136998-A1.

XX 15-JUL-2004.

XX 17-OCT-2003; 2003US-00688015.

XX 30-OCT-2002; 2002US-0422396P.

XX (BAND/) BANDER N H.

XX Bander NH;

XX WPI; 2004-533338/51.

XX Use of anti-prostate specific membrane antigen antibodies for treating or

XX preventing insulin-related disorders, e.g. obesity, hyperglycemia,

XX hyperglycemia, hyperinsulinemia, insulin-resistance, or Type 1 or 2

XX diabetes mellitus.

XX Disclosure; SEQ ID NO 40; 89pp; English.

XX The invention relates to a method of treating or preventing an insulin-

XX related disorder in a subject which comprises administering an antibody

XX or its antigen-binding portion specific for prostate specific membrane

XX antigen (PSMA). The method is useful for treating an insulin-related

XX disorder, including obesity, hyperglycaemia, hypoglycaemia,

XX hyperinsulinaemia, insulin-resistance, impaired glucose tolerance,

XX impaired fasting glucose, Type 1 diabetes mellitus, Type 2 diabetes

XX mellitus, and gestational diabetes. The present sequence represents an

XX artificially deimmunised framework sequence.

Search completed: December 4, 2005, 04:45:01
 Job time : 97.5625 secs

Sequence 11 AA;

Query Match 100.0%; Score 59; DB 8; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTSS 11
 |||||
 Db 1 WGGGTTVTSS 11

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:45 ; Search time 15.5833 Seconds
(without alignments)
67.918 Million cell updates/sec

Title: US-10-632-706-198
Perfect score: 59
Sequence: 1 WGQGTIVTSS 11

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	74	2 S26793	Ig heavy chain V r
2	59	100.0	110	2 PH1655	Ig heavy chain V r
3	59	100.0	113	2 S55533	Ig heavy chain V r
4	59	100.0	113	2 S55535	Ig heavy chain V r
5	59	100.0	113	2 S55530	Ig heavy chain V r
6	59	100.0	113	2 S55534	Ig heavy chain V r
7	59	100.0	113	2 S55528	Ig heavy chain V r
8	59	100.0	113	2 S55532	Ig heavy chain V r
9	59	100.0	113	2 S55531	Ig heavy chain V r
10	59	100.0	114	2 S46392	Ig heavy chain V r
11	59	100.0	114	2 S20707	Ig heavy chain V r
12	59	100.0	115	2 S20706	Ig heavy chain V r
13	59	100.0	116	2 S15672	Ig heavy chain V r
14	59	100.0	116	2 S55542	Ig heavy chain V r
15	59	100.0	117	2 S55541	Ig heavy chain V r
16	59	100.0	118	2 PH1666	Ig heavy chain V r
17	59	100.0	118	2 PH1660	Ig heavy chain V r
18	59	100.0	118	2 S32786	Ig heavy chain (an
19	59	100.0	119	2 PH0961	Ig heavy chain V r
20	59	100.0	120	2 PH1650	Ig heavy chain V r
21	59	100.0	120	2 E49590	Ig heavy chain V r
22	59	100.0	120	2 PD0008	Ig heavy chain V r
23	59	100.0	120	2 S55538	Ig heavy chain V r
24	59	100.0	120	2 S55539	Ig heavy chain V r
25	59	100.0	120	2 S55537	Ig heavy chain V r
26	59	100.0	120	2 S55536	Ig heavy chain V r
27	59	100.0	120	2 S12953	Ig heavy chain V r
28	59	100.0	121	2 S31106	Ig heavy chain - h
29	59	100.0	121	2 S55540	Ig heavy chain V r

30	59	100.0	122	2 E36005	Ig heavy chain V r
31	59	100.0	122	2 PH0958	Ig heavy chain V r
32	59	100.0	123	2 S26794	Ig heavy chain V r
33	59	100.0	124	2 S20775	Ig heavy chain V r
34	59	100.0	125	2 S37455	Ig mu chain - huma
35	59	100.0	125	2 S37455	Ig heavy chain V6
36	59	100.0	127	2 S24689	Ig heavy chain V r
37	59	100.0	127	2 S24689	Ig heavy chain V6
38	59	100.0	128	2 S48797	Ig heavy chain V r
39	59	100.0	131	2 S66537	Ig heavy chain V r
40	59	100.0	132	2 PH0954	Ig heavy chain V r
41	59	100.0	133	2 C33548	Ig heavy chain V-I
42	59	100.0	135	2 B32274	Ig heavy chain pre
43	59	100.0	135	2 S78051	Ig heavy chain pre
44	59	100.0	136	2 PH0960	Ig heavy chain V r
45	59	100.0	137	2 S31676	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S26793
Ig heavy chain V region - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C/Accession: S26793
R/Mottari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A/Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fami
A/Cross-references: UNIPARC:UPI0000115FCA; EMBL:X61019; NID:G32787; PIDN:CAA43353.1; PID
A/Accession: S26793
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-74 <MOR>
A/Cross-references: UNIPARC:UPI0000115FCA; EMBL:X61019; NID:G32787; PIDN:CAA43353.1; PID
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 59; DB 2; Length 74;

Best Local Similarity 100.0%; Pred. No. 0.0021;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTIVTSS 11
Db 64 WGQGTIVTSS 74

RESULT 2

PH1655
Ig heavy chain V region (clone 2B8) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C/Accession: PH1655
J.Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A/Title: The structural basis of germline-encoded VH3 immunoglobulin binding to streptolyo
A/Reference number: PH1642; MUID:93301610; PMID:8315388
A/Accession: PH1655
A/Molecule type: mRNA
A/Residues: 1-110 <HIL>
A/Cross-references: UNIPARC:UPI0000176BDC
A/Experimental source: B cell
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 110;

Best Local Similarity 100.0%; Pred. No. 0.0032;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTIVTSS 11
|||||

Db 100 WGGGTTTVSS 110

RESULT 3

S55533

Ig heavy chain V region pe25 - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000

C/Accession: S55533

R/Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using
utations in the variable region genes.

A/Reference number: S55528; MUID:95239763; PMID:7536850

A/Accession: S55533

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-113 <BOB>

A/Cross-references: UNIPARC:UPI0000116205; EMBL:X82594; NID:9854314; PIDN:CAA57930.1; PI

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F.14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 113;

Best Local Similarity 100.0%; Pred. No. 0.0033;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11

Db 103 WGGGTTTVSS 113

RESULT 4

S55535

Ig heavy chain V region pe23 - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000

C/Accession: S55535

R/Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using
utations in the variable region genes.

A/Reference number: S55528; MUID:95239763; PMID:7536850

A/Accession: S55535

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-113 <BOB>

A/Cross-references: UNIPARC:UPI0000116203; EMBL:X82592; NID:9854310; PIDN:CAA57928.1; PI

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F.14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 113;

Best Local Similarity 100.0%; Pred. No. 0.0033;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11

Db 103 WGGGTTTVSS 113

RESULT 5

S55530

Ig heavy chain V region pe17 - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000

C/Accession: S55530

R/Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using
utations in the variable region genes.

A/Reference number: S55528; MUID:95239763; PMID:7536850

A/Accession: S55530

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-113 <BOB>

A/Cross-references: UNIPARC:UPI00001161FD; EMBL:X82586; NID:9854296; PIDN:CAA57922.1; PI

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F.14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 113;

Best Local Similarity 100.0%; Pred. No. 0.0033;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11

Db 103 WGGGTTTVSS 113

RESULT 6

S55534

Ig heavy chain V region pe15 - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000

C/Accession: S55534

R/Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using
utations in the variable region genes.

A/Reference number: S55528; MUID:95239763; PMID:7536850

A/Accession: S55534

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-113 <BOB>

A/Cross-references: UNIPARC:UPI00001161FC; EMBL:X82584; NID:9854292; PIDN:CAA57920.1; PI

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F.14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 113;

Best Local Similarity 100.0%; Pred. No. 0.0033;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11

Db 103 WGGGTTTVSS 113

RESULT 7

S55528

Ig heavy chain V region (pe16/pe14) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000

C/Accession: S55528; S55529

R/Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using
utations in the variable region genes.

A/Reference number: S55528; MUID:95239763; PMID:7536850

A/Accession: S55528

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-113 <BOB>

A/Cross-references: UNIPARC:UPI00001161FB; EMBL:X82585; NID:9854294; PIDN:CAA57921.1; PI

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotrimer; immunoglobulin

F.14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 113;

Best Local Similarity 100.0%; Pred. No. 0.0033;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WGGGTTVTSS 11
Db 103 WGGGTTVTSS 113

RESULT 8

S55532
Ig heavy chain V region pe19 - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
C/Accession: S55532
R/Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using
utations in the variable region genes.
A/Reference number: S55528; PMID:95239763; PMID:7536850
A/Accession: S55532
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-113 <BOB>
A/Cross-references: UNIPARC:UPI00001161FF; EMBL:X82588; NID:9854300; PIDD:CAA57924.1; P
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTVTSS 11
Db 103 WGGGTTVTSS 113

RESULT 9

S55531
Ig heavy chain V region pe18 - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
C/Accession: S55531
R/Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using
utations in the variable region genes.
A/Reference number: S55528; PMID:95239763; PMID:7536850
A/Accession: S55531
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-113 <BOB>
A/Cross-references: UNIPARC:UPI00001161FF; EMBL:X82587; NID:9854298; PIDD:CAA57923.1; P
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTVTSS 11
Db 103 WGGGTTVTSS 113

RESULT 10.

S46392
Ig heavy chain V region (VH-28) - human
C/Species: Homo sapiens (man)
C/Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C/Accession: S46392
R/Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994

A/Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A/Reference number: S46390; PMID:94254092; PMID:8196048

A/Accession: S46392
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-114 <FIG>
A/Cross-references: UNIPARC:UPI00001137D6; EMBL:Z31688; NID:9499306; PIDD:CAA83493.1; P
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTVTSS 11
Db 104 WGGGTTVTSS 114

RESULT 11

S20707
Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C/Accession: S20707
R/Brenand, D.M.; Hinde, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.; Osbc
submitted to the EMBL Data Library, April 1992
A/Description: Binding specificity and variable region sequences of two monoclonal anticb
A/Reference number: S20706
A/Accession: S20707
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-114 <BRE>
A/Cross-references: UNIPARC:UPI0000176B37; EMBL:Z11916
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F;12-95/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTVTSS 11
Db 104 WGGGTTVTSS 114

RESULT 12

S20706
Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S20706
R/Brenand, D.M.; Hinde, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.; Osbc
submitted to the EMBL Data Library, April 1992
A/Description: Binding specificity and variable region sequences of two monoclonal anticb
A/Reference number: S20706
A/Accession: S20706
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-115 <BRE>
A/Cross-references: UNIPARC:Q8R3V9; UNIPARC:UPI0000176C45; EMBL:Z11914
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F;12-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTVTSS 11
Db 104 WGGGTTVTSS 114

Db 105 WGGTTTVSS 115

RESULT 13

IG heavy chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S15672
R:Tempest, P.R.; Bremner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harris, B.; Technology 9, 266-271, 1991
A>Title: Reshaping a human monoclonal antibody to inhibit human respiratory syncytial virus
A:Reference number: S15672; MUID:91337412; PMID:1367535
A:Accession: S15672
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-116 <TEM>
A:Cross-references: UNIPARC:UPI0000115F4C; EMBL:X58835; NID:951978; PIDN:CAA41644.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGTTTVSS 11
|||||
DB 106 WGGTTTVSS 116

RESULT 14

IG heavy chain V region pe2 - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C:Accession: S55542
R:Boeltger, V.; Boeltger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A>Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using variations in the variable region genes
A:Reference number: S55528; MUID:95239763; PMID:7536850
A:Accession: S55542
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-116 <BOB>
A:Cross-references: UNIPARC:UPI00001161F9; EMBL:X82581; NID:9854302; PIDN:CAA57917.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGTTTVSS 11
|||||
DB 106 WGGTTTVSS 116

RESULT 15

S55541

IG heavy chain V region pe1 - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C:Accession: S55541
R:Boeltger, V.; Boeltger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A>Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using variations in the variable region genes
A:Reference number: S55528; MUID:95239763; PMID:7536850
A:Accession: S55541
A:Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-117 <BOB>
A:Cross-references: UNIPARC:UPI00001161F8; EMBL:X82580; NID:9854286; PIDN:CAA57916.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGTTTVSS 11
|||||
DB 107 WGGTTTVSS 117

Search completed: December 4, 2005, 04:53:46
Job time : 15.5833 secs

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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:08:08 ; Search time 3.20833 Seconds
(without alignments)
16.417 Million cell updates/sec

Title: US-10-632-706-198
Perfect score: 59
Sequence: 1 WGGCTTVTVSS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.New.*
1: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*
2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep.*
5: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
6: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	11	6	US-10-839-799-114
2	59	100.0	11	6	US-10-839-799-129
3	59	100.0	11	7	US-11-108-135-7
4	59	100.0	20	7	US-11-040-159-4
5	59	100.0	20	7	US-11-054-669-107
6	59	100.0	113	7	US-11-144-248-20
7	59	100.0	116	7	US-11-174-186-20
8	59	100.0	116	7	US-11-174-186-21
9	59	100.0	116	7	US-11-174-186-22
10	59	100.0	116	7	US-11-174-186-23
11	59	100.0	116	7	US-11-174-186-24
12	59	100.0	116	7	US-11-174-186-25
13	59	100.0	117	6	US-10-839-799-132
14	59	100.0	117	6	US-11-054-669-120
15	59	100.0	118	6	US-10-932-334-75
16	59	100.0	118	7	US-11-012-353-71
17	59	100.0	120	6	US-10-932-334-71
18	59	100.0	120	7	US-11-096-074-2
19	59	100.0	121	7	US-11-108-135-24
20	59	100.0	124	6	US-10-932-334-13
21	59	100.0	124	7	US-11-144-248-8
22	59	100.0	124	7	US-11-040-159-6
23	59	100.0	124	7	US-11-096-074-14
24	59	100.0	124	7	US-11-096-074-14
25	59	100.0	125	7	US-11-144-248-16

26	59	100.0	125	7	US-11-084-554-8	Sequence 8, Appl1
27	59	100.0	136	6	US-10-839-799-99	Sequence 99, Appl1
28	59	100.0	136	6	US-10-789-273-4	Sequence 4, Appl1
29	59	100.0	143	7	US-11-096-074-6	Sequence 6, Appl1
30	59	100.0	143	7	US-11-096-074-10	Sequence 10, Appl1
31	59	100.0	143	7	US-11-096-074-12	Sequence 12, Appl1
32	59	100.0	143	7	US-11-096-074-16	Sequence 16, Appl1
33	59	100.0	143	7	US-11-096-074-18	Sequence 18, Appl1
34	59	100.0	145	6	US-10-721-763-29	Sequence 29, Appl1
35	59	100.0	154	6	US-10-721-763-25	Sequence 25, Appl1
36	59	100.0	174	7	US-11-144-248-4	Sequence 4, Appl1
37	59	100.0	237	6	US-10-073-301A-9	Sequence 2104, Ap
38	59	100.0	237	7	US-11-054-515-2104	Sequence 2105, Ap
39	59	100.0	240	7	US-11-054-515-2105	Sequence 2113, Ap
40	59	100.0	240	7	US-11-054-515-2113	Sequence 1927, Ap
41	59	100.0	243	7	US-11-054-515-1927	Sequence 1945, Ap
42	59	100.0	243	7	US-11-054-515-1945	Sequence 2058, Ap
43	59	100.0	247	7	US-11-054-515-1434	Sequence 1434, Ap
44	59	100.0	247	7	US-11-054-515-1434	Sequence 1008, Ap
45	59	100.0	248	7	US-11-054-515-1008	

ALIGNMENTS

RESULT 1
US-10-839-799-114
; Publication No. US20050249726A1
; Publicatation No. US20050249726A1
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshihiko
; SATO, Koh
; TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESS: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/839,799
; FILING DATE: 06-May-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,265
; FILING DATE: 09-SEP-1996
; APPLICATION NUMBER: WO PCT/JP94/01763
; FILING DATE: 19-OCT-1994
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELE: 904136
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-10-839-799-114

Query Match 100.0%; Score 59; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. NO. 0.0001;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11
| | | | |
Db 1 WGGGTTTVSS 11

RESULT 2

US-10-839-799-129
; Sequence 129, Application US/10839799
; Publication No. US20050249726A1
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshihiko
; SATO, Koh
; TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/839,799
; FILING DATE: 06-May-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,265
; FILING DATE: 09-SEP-1996
; APPLICATION NUMBER: WO PCT/JP94/01763
; FILING DATE: 19-OCT-1994
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 129:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 129:
US-10-839-799-129

Query Match 100.0%; Score 59; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. NO. 0.0001;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11
| | | | |
Db 1 WGGGTTTVSS 11

RESULT 3

US-11-108-135-7
; Sequence 7, Application US/11108135
; Publication No. US20050260213A1
; GENERAL INFORMATION:
; APPLICANT: Koenig, Scott
; APPLICANT: Verti, Maria Concetta
; APPLICANT: Tuallion, Nadine
; APPLICANT: Bonvini, Ezio
; APPLICANT: Stavenhagen, Jeffrey
; APPLICANT: Rankin, Christopher

; TITLE OF INVENTION: Fc-gamma-RIIb-specific antibodies and methods of use thereof
; FILE REFERENCE: 11183-014-999
; CURRENT APPLICATION NUMBER: US/11/108,135
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/562,804
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: US 60/582,044
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/582,045
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/654,713
; PRIOR FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Framework sequence from human germline VH1-18 and JH6 - FR4
US-11-108-135-7

Query Match 100.0%; Score 59; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. NO. 0.0001;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11
| | | | |
Db 1 WGGGTTTVSS 11

RESULT 4

US-11-040-159-4
; Sequence 4, Application US/11040159
; Publication No. US2005025552A1
; GENERAL INFORMATION:
; APPLICANT: Flynn, Peter
; APPLICANT: Luehrs, Kenneth
; APPLICANT: Ballin, Robert F.
; APPLICANT: Her, Jeng-Hong
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Yarranton, Geoffrey T.
; APPLICANT: Kalobilos, Inc.
; TITLE OF INVENTION: Antibody Specificity Transfer Using Minimal Essential
; FILE REFERENCE: 021167-001730US
; CURRENT APPLICATION NUMBER: US/11/040,159
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US 60/537,364
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/546,216
; PRIOR FILING DATE: 2004-02-23
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:JH6
US-11-040-159-4

Query Match 100.0%; Score 59; DB 7; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
|||||
Db 10 WGGGTTTVSS 20

RESULT 5

US-11-054-669-107
; Sequence 107, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 107
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-107

Query Match 100.0%; Score 59; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
|||||
Db 10 WGGGTTTVSS 20

RESULT 6

US-11-144-248-20
; Sequence 20, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvatan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-20

Query Match 100.0%; Score 59; DB 7; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
|||||
Db 103 WGGGTTTVSS 113

RESULT 7

US-11-174-186-20
; Sequence 20, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiyu
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS VH veneered
US-11-174-186-20

Query Match 100.0%; Score 59; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
|||||
Db 106 WGGGTTTVSS 116

RESULT 8

US-11-174-186-21
; Sequence 21, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiyu
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS de-immunized VH1
US-11-174-186-21

Query Match 100.0%; Score 59; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
|||||
Db 106 WGGGTTTVSS 116

RESULT 9

US-11-174-186-22
; Sequence 22, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:

APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin-Ming
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019
CURRENT APPLICATION NUMBER: US/11/174,186
CURRENT FILING DATE: 2005-07-01
PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.3
SEQ ID NO 22
LENGTH: 116
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: KS de-immunized VH2
US-11-174-186-22

Query Match 100.0%; Score 59; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
|||||
Db 106 WGGGTTTVSS 116

RESULT 10
US-11-174-186-23
Sequence 23, Application US/11174186
Publication No. US20050244418A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin-Ming
APPLICANT: Qian, Xing
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019
CURRENT APPLICATION NUMBER: US/11/174,186
CURRENT FILING DATE: 2005-07-01
PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.3
SEQ ID NO 23
LENGTH: 116
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: KS de-immunized VH3
US-11-174-186-23

Query Match 100.0%; Score 59; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
|||||
Db 106 WGGGTTTVSS 116

RESULT 11
US-11-174-186-24
Sequence 24, Application US/11174186
Publication No. US20050244418A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin-Ming
APPLICANT: Qian, Xing
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019
CURRENT APPLICATION NUMBER: US/11/174,186
CURRENT FILING DATE: 2005-07-01

PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.3
SEQ ID NO 24
LENGTH: 116
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: KS de-immunized VH4
US-11-174-186-24

Query Match 100.0%; Score 59; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
|||||
Db 106 WGGGTTTVSS 116

RESULT 12
US-11-174-186-25
Sequence 25, Application US/11174186
Publication No. US20050244418A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin-Ming
APPLICANT: Qian, Xing
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019
CURRENT APPLICATION NUMBER: US/11/174,186
CURRENT FILING DATE: 2005-07-01
PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.3
SEQ ID NO 25
LENGTH: 116
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: KS de-immunized VH5
US-11-174-186-25

Query Match 100.0%; Score 59; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
|||||
Db 106 WGGGTTTVSS 116

RESULT 13
US-10-839-799-132
Sequence 132, Application US/10839799
Publication No. US20050249726A1
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPE HUMAN ANTIBODY TO HUMAN
MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESSES:
ADDRESS: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/839,799
FILING DATE: 06-May-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265
FILING DATE: 09-SEP-1996
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-10-839-799-132

Query Match 100.0%; Score 59; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.00089;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTSS 11
|||||
Db 107 WGGGTTVTSS 117

RESULT 14
US-11-054-669-120
Sequence 120, Application US/11054669
Publication No. US20050261480A1
GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
FILE REFERENCE: 30219/US/3
CURRENT APPLICATION NUMBER: US/11/054,669
CURRENT FILING DATE: 2005-02-08
PRIOR APPLICATION NUMBER: US 10/194,975
PRIOR FILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 124
SOFTWARE: Patentin version 3.3
SEQ ID NO 120
LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-669-120

Query Match 100.0%; Score 59; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.00089;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTSS 11
|||||
Db 107 WGGGTTVTSS 117

RESULT 15

US-10-932-334-75
Sequence 75, Application US/10932334
Publication No. US20050249728A1
GENERAL INFORMATION:
APPLICANT: Immunogen, Inc.
TITLE OF INVENTION: ANTI-IGF-1 RECEPTOR ANTIBODY
FILE REFERENCE: A8689
CURRENT APPLICATION NUMBER: US/10/932,334
CURRENT FILING DATE: 2004-09-02
PRIOR APPLICATION NUMBER: US/10/729,441
PRIOR FILING DATE: 2003-12-08
PRIOR APPLICATION NUMBER: 10/170,390
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin version 3.2
SEQ ID NO 75
LENGTH: 118
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic antibody structure
US-10-932-334-75

Query Match 100.0%; Score 59; DB 6; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.0009;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTSS 11
|||||
Db 108 WGGGTTVTSS 118

Search completed: December 4, 2005, 04:37:50
Job time : 3.20833 secs

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OW protein - protein search, using sw model

Run on: December 4, 2005, 04:08:08 ; Search time 3.20833 Seconds
(without alignments)
16.417 Million cell updates/sec

Title: US-10-632-706-198
Perfect score: 59
Sequence: 1 WGGCTVTVSS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*
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4: /cgn2_6/ptodata/1/pubpaa/US08_NEM_PUB pep:*
5: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEM_PUB pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEM_PUB pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEM_PUB pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	11	6	US-10-839-799-114
2	59	100.0	11	6	US-10-839-799-129
3	59	100.0	11	7	US-11-108-135-7
4	59	100.0	20	7	US-11-040-159-4
5	59	100.0	20	7	US-11-054-669-107
6	59	100.0	113	7	US-11-144-248-20
7	59	100.0	116	7	US-11-174-186-20
8	59	100.0	116	7	US-11-174-186-21
9	59	100.0	116	7	US-11-174-186-22
10	59	100.0	116	7	US-11-174-186-23
11	59	100.0	116	7	US-11-174-186-24
12	59	100.0	116	7	US-11-174-186-25
13	59	100.0	117	6	US-10-839-799-112
14	59	100.0	117	7	US-11-054-669-120
15	59	100.0	118	6	US-10-932-334-75
16	59	100.0	118	6	US-11-012-353-71
17	59	100.0	120	6	US-10-932-334-71
18	59	100.0	120	7	US-11-096-074-2
19	59	100.0	121	7	US-11-108-135-24
20	59	100.0	124	6	US-10-932-334-13
21	59	100.0	124	7	US-11-144-248-8
22	59	100.0	124	7	US-11-040-159-6
23	59	100.0	124	7	US-11-040-159-8
24	59	100.0	124	7	US-11-096-074-14
25	59	100.0	125	7	US-11-144-248-16

26	59	100.0	125	7	US-11-084-554-8	Sequence 8, Appl1
27	59	100.0	136	6	US-10-839-799-99	Sequence 99, Appl1
28	59	100.0	138	6	US-10-789-273-4	Sequence 4, Appl1
29	59	100.0	143	7	US-11-096-074-6	Sequence 6, Appl1
30	59	100.0	143	7	US-11-096-074-10	Sequence 10, Appl1
31	59	100.0	143	7	US-11-096-074-12	Sequence 12, Appl1
32	59	100.0	143	7	US-11-096-074-16	Sequence 16, Appl1
33	59	100.0	143	7	US-11-096-074-18	Sequence 18, Appl1
34	59	100.0	145	6	US-10-721-763-29	Sequence 29, Appl1
35	59	100.0	154	6	US-10-721-763-25	Sequence 25, Appl1
36	59	100.0	174	7	US-11-144-248-4	Sequence 4, Appl1
37	59	100.0	237	6	US-10-073-301A-9	Sequence 9, Appl1
38	59	100.0	237	7	US-11-054-515-2104	Sequence 2104, Ap
39	59	100.0	240	7	US-11-054-515-2105	Sequence 2105, Ap
40	59	100.0	240	7	US-11-054-515-2113	Sequence 2113, Ap
41	59	100.0	243	7	US-11-054-515-1927	Sequence 1927, Ap
42	59	100.0	243	7	US-11-054-515-1945	Sequence 1945, Ap
43	59	100.0	244	7	US-11-054-515-2058	Sequence 2058, Ap
44	59	100.0	247	7	US-11-054-515-1434	Sequence 1434, Ap
45	59	100.0	248	7	US-11-054-515-1008	Sequence 1008, Ap

ALIGNMENTS

RESULT 1
US-10-839-799-114
Sequence 114, Application US/10839799
Publication No. US20050249726A1
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toeshihiko
SATO, Koh
TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/839, 799
FILING DATE: 06-May-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646, 265
FILING DATE: 09-SEP-1996
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25, 258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-10-839-799-114

Query Match 100.0%; Score 59; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
|||||
DB 1 WGGGTTTVSS 11

RESULT 2

US-10-839-799-129
Sequence 129, Application US/10839799
Publication No. US20050249726A1
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshiniko
SATO, Koh
TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
MEDULOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/839,799
FILING DATE: 06-May-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265
FILING DATE: 09-SEP-1996
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 129:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 129:
US-10-839-799-129

Query Match 100.0%; Score 59; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
|||||
DB 1 WGGGTTTVSS 11

RESULT 3

US-11-108-135-7
Sequence 7, Application US/11108135
Publication No. US20050260213A1
GENERAL INFORMATION:
APPLICANT: Koenig, Scott
Veri, Maria Concetta
APPLICANT: Veri, Maria Concetta
APPLICANT: Tuailon, Nadine
APPLICANT: Bonvini, Ezio
APPLICANT: Stavenhagen, Jeffrey
TITLE OF INVENTION: PC-gamma-Riib-specific antibodies and methods of use thereof
FILE REFERENCE: 11183-014-999

CURRENT APPLICATION NUMBER: US/11/108,135
CURRENT FILING DATE: 2005-04-15
PRIOR APPLICATION NUMBER: US 60/562,804
PRIOR FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 60/582,044
PRIOR FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US 60/582,045
PRIOR FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US 60/654,713
PRIOR FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Framework sequence from human germline VH1-18 and JH6 - FR4
US-11-108-135-7

Query Match 100.0%; Score 59; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
|||||
DB 1 WGGGTTTVSS 11

RESULT 4
US-11-040-159-4
Sequence 4, Application US/11040159
Publication No. US2005025552A1
GENERAL INFORMATION:
APPLICANT: Flynn, Peter
APPLICANT: Luehrs, Kenneth
APPLICANT: Balint, Robert P.
APPLICANT: Her, Jeng-Horng
APPLICANT: Bebbington, Christopher R.
APPLICANT: Yarranton, Geoffrey T.
APPLICANT: Kaloblos, Inc.
TITLE OF INVENTION: Antibody Specificity Transfer Using Minimal Essential
TITLE OF INVENTION: Binding Determinants
FILE REFERENCE: 021167-001730US
CURRENT APPLICATION NUMBER: US/11/040,159
CURRENT FILING DATE: 2005-01-20
PRIOR APPLICATION NUMBER: US 60/537,364
PRIOR FILING DATE: 2004-01-20
PRIOR APPLICATION NUMBER: US 60/546,216
PRIOR FILING DATE: 2004-02-23
NUMBER OF SEQ ID NOS: 133
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: JH6
US-11-040-159-4

Query Match 100.0%; Score 59; DB 7; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11
|||||
Db 10 WGGGTTTVSS 20

RESULT 5

US-11-054-669-107
; Sequence 107, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 107
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-107

Query Match 100.0%; Score 59; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11
|||||
Db 10 WGGGTTTVSS 20

RESULT 6

US-11-144-248-20
; Sequence 20, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-20

Query Match 100.0%; Score 59; DB 7; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11
|||||
Db 103 WGGGTTTVSS 113

RESULT 7
US-11-174-186-20
; Sequence 20, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xingyi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS VH veneered
US-11-174-186-20

Query Match 100.0%; Score 59; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11
|||||
Db 106 WGGGTTTVSS 116

RESULT 8

US-11-174-186-21
; Sequence 21, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xingyi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS de-immunized VH1
US-11-174-186-21

Query Match 100.0%; Score 59; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11
|||||
Db 106 WGGGTTTVSS 116

RESULT 9

US-11-174-186-22
; Sequence 22, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:

APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin-Ming
APPLICANT: Qian, Xingui
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019
CURRENT APPLICATION NUMBER: US/11/174,186
CURRENT FILING DATE: 2005-07-01
PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 22
LENGTH: 116
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: KS de-immunized VH2
US-11-174-186-22

Query Match 100.0%; Score 59; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGTTVTVSS 11
|||||
Db 106 WGGTTVTVSS 116

RESULT 10
US-11-174-186-23
Sequence 23, Application US/11/174186
Publication No. US20050244418A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin-Ming
APPLICANT: Qian, Xingui
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019
CURRENT APPLICATION NUMBER: US/11/174,186
CURRENT FILING DATE: 2005-07-01
PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 23
LENGTH: 116
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: KS de-immunized VH3
US-11-174-186-23

Query Match 100.0%; Score 59; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGTTVTVSS 11
|||||
Db 106 WGGTTVTVSS 116

RESULT 11
US-11-174-186-24
Sequence 24, Application US/11/174186
Publication No. US20050244418A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin-Ming
APPLICANT: Qian, Xingui
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019
CURRENT APPLICATION NUMBER: US/11/174,186
CURRENT FILING DATE: 2005-07-01

PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 24
LENGTH: 116
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: KS de-immunized VH4
US-11-174-186-24

Query Match 100.0%; Score 59; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGTTVTVSS 11
|||||
Db 106 WGGTTVTVSS 116

RESULT 12
US-11-174-186-25
Sequence 25, Application US/11/174186
Publication No. US20050244418A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin-Ming
APPLICANT: Qian, Xingui
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019
CURRENT APPLICATION NUMBER: US/11/174,186
CURRENT FILING DATE: 2005-07-01
PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 25
LENGTH: 116
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: KS de-immunized VH5
US-11-174-186-25

Query Match 100.0%; Score 59; DB 7; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGTTVTVSS 11
|||||
Db 106 WGGTTVTVSS 116

RESULT 13
US-10-839-799-132
Sequence 132, Application US/10839799
Publication No. US20050249726A1
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshitoko
SATO, Koh
TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/839,799
FILING DATE: 06-May-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265
FILING DATE: 09-SEP-1996
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 132:
US-10-839-799-132

Query Match 100.0%; Score 59; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.00089;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
|||
Db 107 WGGGTTTVSS 117

RESULT 14
US-11-054-669-120
Sequence 120, Application US/11054669
Publication No. US20050261480A1
GENERAL INFORMATION:
APPLICANT: Foote, Jefferson
TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
FILE REFERENCE: 30219/US/3
CURRENT APPLICATION NUMBER: US/11/054,669
CURRENT FILING DATE: 2005-02-08
PRIOR APPLICATION NUMBER: US 10/194,975
PRIOR FILING DATE: 2002-07-12
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 124
SOFTWARE: Patent version 3.3
SEQ ID NO 120
LENGTH: 117
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-669-120

Query Match 100.0%; Score 59; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.00089;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
|||
Db 107 WGGGTTTVSS 117

RESULT 15

US-10-932-334-75
Sequence 75, Application US/10932334
Publication No. US20050249728A1
GENERAL INFORMATION:
APPLICANT: Immunogen, Inc.
TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
FILE REFERENCE: A8689
CURRENT APPLICATION NUMBER: US/10/932,334
CURRENT FILING DATE: 2004-09-02
PRIOR APPLICATION NUMBER: US/10/729,441
PRIOR FILING DATE: 2003-12-08
PRIOR APPLICATION NUMBER: 10/170,390
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patent version 3.2
SEQ ID NO 75
LENGTH: 118
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic antibody structure
US-10-932-334-75

Query Match 100.0%; Score 59; DB 6; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.0009;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
|||
Db 108 WGGGTTTVSS 118

Search completed: December 4, 2005, 04:37:50
Job time: 3.20833 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:07:28 ; Search time 78.8333 Seconds
(without alignments)
58.302 Million cell updates/sec

Title: US-10-632-706-198
Perfect score: 59
Sequence: 1 WQGTITVTVSS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_MA_Main:*

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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	11	3	US-09-253-794-40 Sequence 40, App1
2	59	100.0	11	3	US-09-828-708-78 Sequence 78, App1
3	59	100.0	11	3	US-09-749-873-114 Sequence 114, App1
4	59	100.0	11	3	US-09-749-873-114 Sequence 129, App1
5	59	100.0	11	3	US-09-263-921-137 Sequence 137, App1
6	59	100.0	11	3	US-09-563-222-157 Sequence 157, App1
7	59	100.0	11	3	US-09-563-222-157 Sequence 165, App1
8	59	100.0	11	3	US-09-563-222-181 Sequence 181, App1
9	59	100.0	11	3	US-09-563-222-197 Sequence 179, App1
10	59	100.0	11	3	US-09-509-098-179 Sequence 179, App1
11	59	100.0	11	4	US-10-218-253-137 Sequence 137, App1
12	59	100.0	11	4	US-10-169-351-4 Sequence 4, App11
13	59	100.0	11	4	US-10-160-506-40 Sequence 40, App11
14	59	100.0	11	4	US-10-310-113-26 Sequence 26, App1
15	59	100.0	11	4	US-10-310-113-147 Sequence 147, App1
16	59	100.0	11	4	US-10-310-113-148 Sequence 148, App1
17	59	100.0	11	4	US-10-310-113-149 Sequence 149, App1
18	59	100.0	11	4	US-10-310-113-150 Sequence 150, App1
19	59	100.0	11	4	US-10-310-113-151 Sequence 151, App1
20	59	100.0	11	4	US-10-310-113-152 Sequence 152, App1
21	59	100.0	11	4	US-10-310-113-153 Sequence 153, App1
22	59	100.0	11	4	US-10-310-113-154 Sequence 154, App1
23	59	100.0	11	4	US-10-310-113-155 Sequence 155, App1
24	59	100.0	11	4	US-10-310-113-156 Sequence 156, App1
25	59	100.0	11	4	US-10-310-113-157 Sequence 157, App1
26	59	100.0	11	4	US-10-310-113-158 Sequence 158, App1
27	59	100.0	11	4	US-10-310-113-159 Sequence 159, App1

28	59	100.0	11	4	US-10-412-703A-135 Sequence 135, App1
29	59	100.0	11	4	US-10-443-466A-69 Sequence 69, App1
30	59	100.0	11	4	US-10-443-466A-120 Sequence 120, App1
31	59	100.0	11	4	US-10-449-379-40 Sequence 40, App1
32	59	100.0	11	4	US-10-688-015-40 Sequence 40, App1
33	59	100.0	11	4	US-10-632-706-195 Sequence 195, App1
34	59	100.0	11	4	US-10-632-706-198 Sequence 198, App1
35	59	100.0	11	4	US-10-632-706-201 Sequence 201, App1
36	59	100.0	11	4	US-10-632-706-204 Sequence 204, App1
37	59	100.0	11	4	US-10-783-950-146 Sequence 146, App1
38	59	100.0	11	4	US-10-783-950-169 Sequence 169, App1
39	59	100.0	11	4	US-10-160-505-40 Sequence 40, App1
40	59	100.0	11	5	US-10-751-826-120 Sequence 120, App1
41	59	100.0	11	5	US-10-923-068-113 Sequence 113, App1
42	59	100.0	11	5	US-10-630-009-78 Sequence 78, App1
43	59	100.0	11	5	US-10-785-382-40 Sequence 40, App1
44	59	100.0	11	5	US-10-984-960A-9 Sequence 9, App11
45	59	100.0	11	5	US-10-984-960A-45 Sequence 45, App1

ALIGNMENTS

RESULT 1
US-09-253-794-40
Sequence 40, Application US/09253794
Patent No. US20020018750A1
GENERAL INFORMATION:
APPLICANT: HANSEN, Hans J.
ARMOUR, Kathryn L.
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED MOUSE MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/253,794
FILING DATE: 22-Feb-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,157
FILING DATE: 05-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/464
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-253-794-40
Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11
|||
Db 1 WGGGTTTVSS 11

RESULT 2
US-09-828-708-78
Sequence 78, Application US/09828708
Patent No. US20020146753A1
GENERAL INFORMATION:
APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
FILE REFERENCE: 1361.005US1
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 78
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-708-78

Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11
|||
Db 1 WGGGTTTVSS 11

RESULT 3
US-09-749-873-114
Sequence 114, Application US/09749873
Publication No. US20030023045A1
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
SATO, Koh
TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/749,873
FILING DATE: 29-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,265
FILING DATE: 1996-09-09
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-09-749-873-114

Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11
|||
Db 1 WGGGTTTVSS 11

RESULT 4
US-09-749-873-129
Sequence 129, Application US/09749873
Publication No. US20030023045A1
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshihiko
SATO, Koh
TSUCHIYA, Masayuki

TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
MEDULLOBLASTOMA CELLS

NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/749,873
FILING DATE: 29-Dec-2000

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,265
FILING DATE: 1996-09-09

APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258

REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399

INFORMATION FOR SEQ ID NO: 129:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 129:
US-09-749-873-129

Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTVTSS 11
| | | | |
Db 1 WGGGTTVTSS 11

RESULT 5

US-09-269-921-137
; Sequence 137, Application US/09269921
; Publication No. US20030045691A1
; GENERAL INFORMATION:
; APPLICANT: Ono, Koichiro
; APPLICANT: Ohtomo, Toshiniko
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yoshimura, Yasushi
; APPLICANT: Koshihara, Yasuo
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-FM 1.24 ANTIBODY
; FILE REFERENCE: 35029-20007.00
; CURRENT FILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: PCT/JP97/03553
; EARLIER FILING DATE: 1997-10-03
; EARLIER APPLICATION NUMBER: JP 8-264756
; EARLIER FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: JH6
; PUBLICATION INFORMATION:
; AUTHORS: Ravetch, J. et al.
; JOURNAL: CELL
; VOLUME: 27
; PAGES: 583-591
; DATE: 1981
US-09-269-921-137

Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTVTSS 11
| | | | |
Db 1 WGGGTTVTSS 11

RESULT 6

US-09-563-222-157
; Sequence 157, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-157

Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTVTSS 11
| | | | |
Db 1 WGGGTTVTSS 11

RESULT 7

US-09-563-222-165
; Sequence 165, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-165

Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTVTSS 11
| | | | |
Db 1 WGGGTTVTSS 11

RESULT 8

US-09-563-222-181
; Sequence 181, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 181
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-181

Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTVTSS 11
| | | | |
Db 1 WGGGTTVTSS 11

RESULT 9

US-09-563-222-197
; Sequence 197, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406

;; CURRENT APPLICATION NUMBER: US/09/563,222
;; CURRENT FILING DATE: 2000-05-02
;; NUMBER OF SEQ ID NOS: 197
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 197
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-09-563-222-197

Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11
Db 1 WGGGTTTVSS 11

RESULT 10
US-09-509-098-179
;; Sequence 179, Application US/09509098
;; Publication No. US20030103970A1
;; GENERAL INFORMATION:
;; APPLICANT: TSUCHIYA, MASAYUKI
;; TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
;; FILE REFERENCE: 053466/0274
;; CURRENT APPLICATION NUMBER: US/09/509,098
;; PRIOR FILING DATE: 2000-03-22
;; PRIOR APPLICATION NUMBER: PCT/J998/04469
;; PRIOR FILING DATE: 1998-10-02
;; PRIOR APPLICATION NUMBER: JP 9-271726
;; PRIOR FILING DATE: 1997-10-03
;; NUMBER OF SEQ ID NOS: 203
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 179
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
US-09-509-098-179

Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11
Db 1 WGGGTTTVSS 11

RESULT 11
US-10-218-253-137
;; Sequence 137, Application US/10218253
;; Publication No. US20030129185A1
;; GENERAL INFORMATION:
;; APPLICANT: Ono, Koichiro
;; APPLICANT: Ohmoto, Toshihiko
;; APPLICANT: Tsuchiya, Masayuki
;; APPLICANT: Yoshimura, Yasushi
;; APPLICANT: Koshihara, Yasuo
;; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
;; FILE REFERENCE: 35029-20007.00
;; CURRENT APPLICATION NUMBER: US/10/218,253
;; CURRENT FILING DATE: 2002-11-21
;; PRIOR APPLICATION NUMBER: US/09/269,921
;; PRIOR FILING DATE: 1999-04-01
;; PRIOR APPLICATION NUMBER: PCT/J997/03553
;; PRIOR FILING DATE: 1997-10-03
;; PRIOR APPLICATION NUMBER: JP 8-264756
;; PRIOR FILING DATE: 1996-10-04

;; NUMBER OF SEQ ID NOS: 137
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 137
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Unknown
;; FEATURE:
;; OTHER INFORMATION: Description of Unknown Organism: JH6
;; PUBLICATION INFORMATION:
;; AUTHORS: Ravetch, J. et al.
;; JOURNAL: CELL
;; VOLUME: 27
;; PAGES: 583-591
;; DATE: 1981
US-10-218-253-137

Query Match 100.0%; Score 59; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11
Db 1 WGGGTTTVSS 11

RESULT 12
US-10-169-351-4
;; Sequence 4, Application US/10169351
;; Publication No. US20030157090A1
;; GENERAL INFORMATION:
;; APPLICANT: BENVENTO, EUGENIO
;; APPLICANT: FRANCONI, ROSELLA
;; APPLICANT: DESIDERIO, ANGIOLA
;; APPLICANT: TAVLADORAKI, PARASKEVI
;; TITLE OF INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANTIBODIES
;; TITLE OF INVENTION: WHICH INCLUDE THEM
;; FILE REFERENCE: 4161-4
;; CURRENT APPLICATION NUMBER: US/10/169,351
;; CURRENT FILING DATE: 2002-10-29
;; PRIOR APPLICATION NUMBER: PCT/IT00/00554
;; PRIOR FILING DATE: 2000-12-29
;; PRIOR APPLICATION NUMBER: IT RM99A000803
;; PRIOR FILING DATE: 1999-12-30
;; NUMBER OF SEQ ID NOS: 118
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 4
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-169-351-4

Query Match 100.0%; Score 59; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11
Db 1 WGGGTTTVSS 11

RESULT 13
US-10-160-506-40
;; Sequence 40, Application US/10160506
;; Publication No. US20030161832A1
;; GENERAL INFORMATION:
;; APPLICANT: Bander, Neil H.
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
;; TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR
;; FILE REFERENCE: 10448-162001


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; CURRENT APPLICATION NUMBER: US/10/160,506
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/324,100
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/362,612
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: deimmunized heavy chain v415-4
US-10-160-506-40

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Query Match          100.0%; Score 59; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 WGGGTTTVSS 11
        |||||
Db       1 WGGGTTTVSS 11

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RESULT 14
US-10-310-113-26
; Sequence 26, Application US/10310113
; Publication No. US2003017664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; APPLICANT: NIEVES, ESPERANZA LILIANA
; APPLICANT: MOSQUERA, LUIS A.
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/310,113
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-310-113-26

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Query Match          100.0%; Score 59; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 WGGGTTTVSS 11
        |||||
Db       1 WGGGTTTVSS 11

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RESULT 15
US-10-310-113-147
; Sequence 147, Application US/10310113
; Publication No. US2003017664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; APPLICANT: NIEVES, ESPERANZA LILIANA
; APPLICANT: MOSQUERA, LUIS A.

```

```

; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; TITLE OF INVENTION: THROMBOSES
; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/310,113
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 147
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: humanized HC-01 FR4 amino acid sequence
US-10-310-113-147

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Query Match          100.0%; Score 59; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 WGGGTTTVSS 11
        |||||
Db       1 WGGGTTTVSS 11

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Search completed: December 4, 2005, 04:37:44
Job time : 79.8333 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 03:59:51 ; Search time 23.6042 Seconds
(without alignments)
38.528 Million cell updates/sec

Title: US-10-632-706-198
Perfect score: 59
Sequence: 1 WGGGTWTVSS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5 COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/6 COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/H COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/PTTUS COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/RE COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfills1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	11	1	US-08-471-780C-120 Sequence 120, App
2	59	100.0	11	1	US-08-467-282B-120 Sequence 120, App
3	59	100.0	11	1	US-08-471-282A-120 Sequence 120, App
4	59	100.0	11	1	US-08-318-157B-40 Sequence 40, Appl
5	59	100.0	11	1	US-08-466-710C-120 Sequence 120, App
6	59	100.0	11	2	US-08-468-738C-120 Sequence 120, App
7	59	100.0	11	2	US-08-646-265A-114 Sequence 114, App
8	59	100.0	11	2	US-08-646-265A-114 Sequence 129, App
9	59	100.0	11	2	US-09-253-794-40 Sequence 40, Appl
10	59	100.0	11	2	US-09-563-222C-146 Sequence 146, App
11	59	100.0	11	2	US-09-563-222C-169 Sequence 169, App
12	59	100.0	11	2	US-09-263-921-137 Sequence 137, App
13	59	100.0	11	2	US-09-293-769A-120 Sequence 120, App
14	59	100.0	13	6	5189147-14 Patent No. 5189147
15	59	100.0	15	6	5189147-179B-8 Patent No. 5189147
16	59	100.0	15	6	5189147-20 Patent No. 5189147
17	59	100.0	16	4	PCT-US91-02942-91 Patent No. 5189147
18	59	100.0	20	2	US-10-194-975-107 Sequence 91, Appl
19	59	100.0	22	4	PCT-US91-02942-100 Sequence 107, App
20	59	100.0	29	1	US-08-053-131-73 Sequence 100, App
21	59	100.0	29	1	US-08-645-641-73 Sequence 73, Appl
22	59	100.0	29	1	US-07-853-408B-73 Sequence 73, Appl
23	59	100.0	29	1	US-08-096-762-73 Sequence 73, Appl
24	59	100.0	29	1	US-08-308-865-73 Sequence 73, Appl
25	59	100.0	29	2	US-09-042-353-270 Sequence 270, App
26	59	100.0	29	2	US-08-758-417A-118 Sequence 118, App
27	59	100.0	29	4	PCT-US92-10983-73 Sequence 73, Appl

28	59	100.0	31	1	US-08-053-131-83 Sequence 83, Appl
29	59	100.0	31	1	US-08-645-641-83 Sequence 83, Appl
30	59	100.0	31	1	US-07-853-408B-83 Sequence 83, Appl
31	59	100.0	31	1	US-08-096-762-83 Sequence 83, Appl
32	59	100.0	31	1	US-08-308-865-83 Sequence 83, Appl
33	59	100.0	31	2	US-09-042-353-280 Sequence 280, App
34	59	100.0	31	2	US-08-758-417A-128 Sequence 128, App
35	59	100.0	31	4	PCT-US92-10983-83 Sequence 83, Appl
36	59	100.0	32	1	US-08-053-131-92 Sequence 92, Appl
37	59	100.0	32	1	US-08-645-641-92 Sequence 92, Appl
38	59	100.0	32	1	US-07-853-408B-92 Sequence 92, Appl
39	59	100.0	32	1	US-08-096-762-92 Sequence 92, Appl
40	59	100.0	32	1	US-08-308-865-92 Sequence 92, Appl
41	59	100.0	32	2	US-09-042-353-289 Sequence 289, App
42	59	100.0	32	2	US-08-758-417A-137 Sequence 137, App
43	59	100.0	32	4	PCT-US92-10983-92 Sequence 92, Appl
44	59	100.0	33	1	US-08-053-131-89 Sequence 89, Appl
45	59	100.0	33	1	US-08-645-641-89 Sequence 89, Appl

ALIGNMENTS

RESULT 1
US-08-471-780C-120
; Sequence 120, Application US/08471780C
; Patent No. 5759808
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,780C
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane B.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 120:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-471-780C-120
; Query Match 100.0%; Score 59; DB 1; Length 11;
; Best Local Similarity 100.0%; Pred. No. 0.0017;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WGGGTTTVSS 11
|||
Db 1 WGGGTTTVSS 11

RESULT 2
US-08-467-282B-120
; Sequence 120, Application US/08467282B
; Patent No. 5800988
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,282B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958-0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 120:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-467-282B-120
Query Match 100.0%; Score 59; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WGGGTTTVSS 11
|||
Db 1 WGGGTTTVSS 11

RESULT 3
US-08-471-282A-120
; Sequence 120, Application US/08471282A
; Patent No. 5840853
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,282A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958-0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 120:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-471-282A-120

Query Match 100.0%; Score 59; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WGGGTTTVSS 11
|||
Db 1 WGGGTTTVSS 11

RESULT 4
US-08-318-157B-40
; Sequence 40, Application US/08318157B
; Patent No. 5874540
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; APPLICANT: ARMOIR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,157B
; FILING DATE: 05-OCT-1994

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/464
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-318-157B-40

Query Match 100.0%; Score 59; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGTTTVSS 11
|||
Db 1 WGGTTTVSS 11

RESULT 5
US-08-466-710C-120
Sequence 120, Application US/08466710C
Patent No. 5874541
GENERAL INFORMATION:
APPLICANT: Casterman, Cecile
APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,710C
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-466-710C-120

Query Match 100.0%; Score 59; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGTTTVSS 11
|||
Db 1 WGGTTTVSS 11

RESULT 6
US-08-468-739C-120
Sequence 120, Application US/08468739C
Patent No. 6015695
GENERAL INFORMATION:
APPLICANT: Casterman, Cecile
APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,739C
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-468-739C-120

Query Match 100.0%; Score 59; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGTTTVSS 11
|||
Db 1 WGGTTTVSS 11

RESULT 7
US-08-646-265A-114
Sequence 114, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:

APPLICANT: OHTOMO, Toshiniko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-646-265A-114

Query Match 100.0%; Score 59; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11
|||
Db 1 WGGGTTTVSS 11

RESULT 8
US-08-646-265A-129
Sequence 129, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshiniko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULLOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 129:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-646-265A-129

Query Match 100.0%; Score 59; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11
|||
Db 1 WGGGTTTVSS 11

RESULT 9
US-09-253-794-40
Sequence 40, Application US/09253794
Patent No. 6676324
GENERAL INFORMATION:
APPLICANT: HANSEN, Hans J.
ARMOUR, Kathryn L.
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
MOUSE MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/253,794
FILING DATE: 22-Feb-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,157
FILING DATE: 05-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/464
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-253-794-40

Query Match 100.0%; Score 59; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
|||
Db 1 WGGGTTTVSS 11

RESULT 10
US-09-563-222C-146
Sequence 146, Application US/09563222C
Patent No. 6696620
GENERAL INFORMATION:
APPLICANT: EPICYTE PHARMACEUTICALS, INC.
APPLICANT: HIATT, ANDREW C.
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
FILE REFERENCE: 068904-0501
CURRENT APPLICATION NUMBER: US/09/563,222C
CURRENT FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: PCT/US01/14349
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/563,222
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 146
LENGTH: 11
TYPE: PRT
ORGANISM: Mus musculus
US-09-563-222C-146

Query Match 100.0%; Score 59; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
|||
Db 1 WGGGTTTVSS 11

RESULT 11
US-09-563-222C-169
Sequence 169, Application US/09563222C
Patent No. 6696620
GENERAL INFORMATION:
APPLICANT: EPICYTE PHARMACEUTICALS, INC.
APPLICANT: HIATT, ANDREW C.
APPLICANT: HEIN, MICHAEL B.
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
FILE REFERENCE: 068904-0501
CURRENT APPLICATION NUMBER: US/09/563,222C
CURRENT FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: PCT/US01/14349
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/563,222
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 169

LENGTH: 11
TYPE: PRT
ORGANISM: Mus musculus
US-09-563-222C-169

Query Match 100.0%; Score 59; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
|||
Db 1 WGGGTTTVSS 11

RESULT 12
US-09-269-921-137
Sequence 137, Application US/09269921
Patent No. 6699974
GENERAL INFORMATION:
APPLICANT: Ono, Koichiro
APPLICANT: Tsuchiya, Masayuki
APPLICANT: Yoshimura, Yasuo
TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
FILE REFERENCE: 35029-20007.00
CURRENT APPLICATION NUMBER: US/09/269,921
CURRENT FILING DATE: 1999-04-01
EARLIER APPLICATION NUMBER: PCT/JP97/03553
EARLIER FILING DATE: 1997-10-03
EARLIER APPLICATION NUMBER: JP 8-264756
EARLIER FILING DATE: 1996-10-04
NUMBER OF SEQ ID NOS: 137
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 137
LENGTH: 11
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: JH6
PUBLICATION INFORMATION:
AUTHORS: Ravetch, J. et al.
JOURNAL: CELL
VOLUME: 27
PAGES: 583-591
DATE: 1981
US-09-269-921-137

Query Match 100.0%; Score 59; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
|||
Db 1 WGGGTTTVSS 11

RESULT 13
US-09-293-769A-120
Sequence 120, Application US/09293769A
Patent No. 6765087
GENERAL INFORMATION:
APPLICANT: CASTERMAN, CECILE
APPLICANT: HAWERS, RAYMOND
TITLE OF INVENTION: IMMUNOGLOBULINS DEVOID OF LIGHT CHAINS
FILE REFERENCE: 04958.0008-07000
CURRENT APPLICATION NUMBER: US/09/293,769A
CURRENT FILING DATE: 1999-04-19
PRIOR APPLICATION NUMBER: 08/471,284
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 07/106,944
PRIOR FILING DATE: 1987-10-15
PRIOR APPLICATION NUMBER: EPO 92402326.0

;; PRIOR FILING DATE: 1992-08-21
;; PRIOR APPLICATION NUMBER: EPO 93401310.3
;; PRIOR FILING DATE: 1993-05-21
;; NUMBER OF SEQ ID NOS: 130
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 120
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-293-769A-120

Query Match 100.0%; Score 59; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WGGGTTTVSS 11
Db 1 WGGGTTTVSS 11

RESULT 14
5189147-14
; Patent No. 5189147
; APPLICANT: SAITO, HARUO; KRANZ, DAVID M.; EISEN, HERMAN N.;
; TONEGAWA, SUSUMU
; TITLE OF INVENTION: METERODIMERIC T LYMPHOCYTE RECEPTOR
; ANTI BODY
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/271,216
; FILING DATE: 14-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 666,988
; FILING DATE: 31-OCT-1984
; APPLICATION NUMBER: 620,122
; FILING DATE: 13-JUN-1984
; SEQ ID NO: 14:
; LENGTH: 13
5189147-14

Query Match 100.0%; Score 59; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WGGGTTTVSS 11
Db 3 WGGGTTTVSS 13

RESULT 15
US-08-765-179B-8
; Sequence 8, Application US/08765179B
; Patent No. 5854027
; GENERAL INFORMATION:
; APPLICANT: STEIBE, Boris
; APPLICANT: STEINBACHER, Stefan
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY
; TITLE OF INVENTION: OF ANTIBODIES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,179B

;; FILING DATE: 14-JAN-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/EP95/02626
;; FILING DATE: 06-JUL-1995
;; PRIOR APPLICATION DATA: DE P 44 25 115.7
;; FILING DATE: 15-JUL-1994
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-765-179B-8

Query Match 100.0%; Score 59; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WGGGTTTVSS 11
Db 5 WGGGTTTVSS 15

Search completed: December 4, 2005, 04:09:45
Job time : 24.6042 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:09:54 ; Search time 95.5625 Seconds
(without alignments)
50.576 Million cell updates/sec

Title: US-10-632-706-127
Perfect score: 60
Sequence: 1 LATYYFGLDV 11

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	11	8	ADR38724 Mouse hea
2	60	100.0	11	8	ADR38725 Mouse hea
3	48	80.0	122	9	AEb45960 Human mon
4	47	78.3	114	7	ADD28082 Lymphoma
5	47	78.3	129	7	ADD28323 Human het
6	47	78.3	134	7	ADD28237 Human het
7	47	78.3	134	9	ADV86824 Bacillus
8	47	78.3	244	8	ADR28082 NPB polyp
9	47	78.3	468	9	AEb45891 Human mon
10	46	76.7	469	9	AEb45853 Human mon
11	46	76.7	13	8	ADR38712 Mouse hea
12	46	76.7	21	9	ADM04816 PAPP-A im
13	46	76.7	126	9	AD241994 Ig H chai
14	46	76.7	140	9	ADM04810 PAPP-A im
15	45	75.0	16	9	ADM04952 PAPP-A im
16	45	75.0	21	5	ABP47057 Human Bly
17	45	75.0	21	7	ADG97884 scfV VHCD
18	45	75.0	24	9	ADM77426 Human pla
19	45	75.0	117	9	AEb01019 Human hea
20	45	75.0	135	9	ADM04946 PAPP-A im
21	45	75.0	256	9	ABP45889 Human Bly
22	45	75.0	256	7	ADG96416 Single ch
23	44	73.3	13	4	AAU02710 CDR regio
24	44	73.3	14	9	ADY70216 Human Mab

25	44	73.3	16	5	ABP46118 Human Bly
26	44	73.3	16	7	ADG96945 scfV VHCD
27	44	73.3	17	5	ABP46865 Human Bly
28	44	73.3	17	7	ADG97692 scfV VHCD
29	44	73.3	18	9	AEa21444 Human ant
30	44	73.3	109	8	AD105782 Human mon
31	44	73.3	117	7	ADK18782 Anti-huma
32	44	73.3	122	4	AAU02589 Anti-adip
33	44	73.3	123	7	ADP03879 Murine-ex
34	44	73.3	123	7	ADP03878 Murine-ex
35	44	73.3	123	9	ADY70198 Human mon
36	44	73.3	127	5	ABG76565 HCV E1 an
37	44	73.3	127	7	ADK18819 Anti-huma
38	44	73.3	127	7	ADK18901 Anti-huma
39	44	73.3	127	7	ADK18607 Anti-huma
40	44	73.3	127	8	AD125432 Human mAb
41	44	73.3	127	9	AEa21438 Human ant
42	44	73.3	129	7	ADDE28407 Human ant
43	44	73.3	134	7	ADD28238 Human het
44	44	73.3	134	7	ADD28332 Human het
45	44	73.3	134	7	ADD28331 Human het

ALIGNMENTS

RESULT 1
ADR38724 standard; peptide; 11 AA.
AC ADR38724;
XX
XX
DT 02-DEC-2004 (first entry)
XX
XX Mouse heavy chain variable region CDR3 seqid 126.
DE
XX
XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;
KW heavy chain variable region; complementarily determining region; CDR3.
OS Mus sp.
XX
XX US2004175385-A1.
XX
XX
XX 09-SEP-2004.
XX
XX 01-AUG-2003; 2003US-00632706.
XX
XX 31-AUG-1998; 98US-00144886.
XX 01-AUG-2002; 2002US-0400721P.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Marks JD, Amersdorfer P;
XX WPI: 2004-652009/63.
XX
XX New isolated antibody that neutralizes botulinum neurotoxin type A,
XX useful for diagnosing botulism or for treating pathologies associated
XX with botulinum neurotoxin poisoning.
XX
XX Example 3; SEQ ID NO 126; 110pp; English.
XX
XX The invention describes an isolated antibody (I) that specifically binds
XX to an epitope specifically bound by an antibody expressed by a specific
XX clone where (II) binds to and neutralizes botulinum neurotoxin type A
XX (BONT/A). An isolated antibody (I) that specifically binds to an epitope
XX specifically bound by an antibody expressed by a clone chosen from clone
XX S25, C25, C35, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
XX 3-8, 3-10 and INGI, where (II) binds to and neutralizes botulinum
XX neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
XX comprising BONT/A neutralising epitope having an epitope that is

specifically bound by an antibody expressed by clones as mentioned in (I)
; producing (I); and a composition (III) comprising several anti-
botulinum neurotoxin antibodies, where each antibody is specific for a
different epitope of a botulinum neurotoxin and the combination of
antibodies shows greater toxin neutralisation than the single antibodies
in surplus. The following are disclosed: a pharmaceutical composition
comprising (I); and a kit comprising (I). (I) is useful for neutralising
BONT/A antibody and for neutralising a botulinum neurotoxin which
involves contacting neurotoxin with (I) in surplus, where each of (I) is
specific for a different epitope of the botulinum neurotoxin and the
combination of antibodies shows greater toxin neutralisation than the
single antibodies in surplus. (I) is useful for diagnosing the botulinum
or for treating pathologies associated with botulinum neurotoxin
poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
enables rapid detection or diagnosis of botulism. This is the amino acid
sequence of mouse heavy chain variable region complementarity determining
region 3 (CDR3) from anti-botulinum neurotoxin antibodies.

XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 60; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LATYYFGLDV 11
| | | | | | | | | |
Db 1 LATYYFGLDV 11

RESULT 2
ADR38725 standard; peptide; 11 AA.
XX
AC ADR38725;
XX
DT 02-DEC-2004 (first entry)
XX
DS Mouse heavy chain variable region CDR3 seqid 127.
XX
KM antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
KM BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KM toxin neutralisation; botulinum neurotoxin poisoning; mouse;
KM heavy chain variable region; complementarity determining region; CDR3.
XX
OS Mus sp.
XX
PN US2004175385-A1.
XX
PD 09-SEP-2004.
XX
PF 01-AUG-2003; 2003US-00632706.
XX
PR 31-AUG-1998; 98US-00144886.
XX
PR 01-AUG-2002; 2002US-0400721P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Marks JD, Amersdorfer P;
XX
DR WPI; 2004-652009/63.
XX
PT New isolated antibody that neutralizes botulinum neurotoxin type A,
PT useful for diagnosing botulism or for treating pathologies associated
PT with botulinum neurotoxin poisoning.
XX
PS Example 3, SEQ ID NO 127; 110pp; English.
XX
CC The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralises botulinum neurotoxin type A
CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC S25, C35, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,

3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
comprising BONT/A neutralising epitope having an epitope that is
specifically bound by an antibody expressed by clones as mentioned in (I)
; producing (I); and a composition (III) comprising several anti-
botulinum neurotoxin antibodies, where each antibody is specific for a
different epitope of a botulinum neurotoxin and the combination of
antibodies shows greater toxin neutralisation than the single antibodies
in surplus. The following are disclosed: a pharmaceutical composition
comprising (I); and a kit comprising (I). (I) is useful for neutralising
BONT/A antibody and for neutralising a botulinum neurotoxin which
involves contacting neurotoxin with (I) in surplus, where each of (I) is
specific for a different epitope of the botulinum neurotoxin and the
combination of antibodies shows greater toxin neutralisation than the
single antibodies in surplus. (I) is useful for diagnosing the botulinum
or for treating pathologies associated with botulinum neurotoxin
poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
enables rapid detection or diagnosis of botulism. This is the amino acid
sequence of mouse heavy chain variable region complementarity determining
region 3 (CDR3) from anti-botulinum neurotoxin antibodies.

XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 60; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LATYYFGLDV 11
| | | | | | | | | |
Db 1 LATYYFGLDV 11

RESULT 3
ABE45960 standard; protein; 122 AA.
XX
AC ABE45960;
XX
DT 06-OCT-2005 (first entry)
XX
DE Human monoclonal anti-MADCAM antibody related protein #4.
XX
KM Monoclonal antibody; mucosal addressin cell adhesion molecule; MADCAM;
KM inflammation; inflammatory bowel disease; Crohns disease;
KM ulcerative colitis; diverticular disease; gastritis; liver disease;
KM primary biliary cirrhosis; primary sclerosing cholangitis;
KM insulin dependent diabetes; graft versus host disease; anti-inflammatory;
KM gastrointestinal-gen.; antidiabetic; hepatotropic; antidiabetic;
KM immunosuppressive; antibody.
XX
OS Homo sapiens.
XX
PN WO2005067620-A2.
XX
PD 28-JUL-2005.
XX
PF 07-JAN-2005; 2005WO-US000370.
XX
PR 09-JAN-2004; 2004US-0535490P.
XX
PA (PFI2) PRIZER INC.
XX
PA (ABGE-) ABGENIX INC.
XX
PI (PFI2) PRIZER LTD.
XX
PI Pullen N, Molloy E, Kellermann S, Green IL, Haek-Frendscho M,
XX
DR WPI; 2005-554958/56.
XX
CC New antibody to Mucosal Adressin Cell Adhesion Molecule, useful for
CC diagnosing and treating an inflammatory disease, e.g. inflammatory bowel
CC disease, ulcerative colitis, gastritis, insulin-dependent diabetes or
CC graft versus host disease.

PS Example 5; Fig 1; 167pp; English.

XX The invention relates to a human monoclonal antibody or its antigen-
 CC binding portion that specifically binds to mucosal addressin cell
 CC adhesion molecule (MAdCAM). The invention also relates to a hybridoma
 CC cell line that produces the human monoclonal antibody, a pharmaceutical
 CC composition comprising an amount of the monoclonal antibody or its
 CC antigen-binding portion and a pharmaceutical carrier, a method of
 CC treating inflammatory disease in a subject, an isolated cell line that
 CC produces the monoclonal antibody or its antigen-binding portion or the
 CC heavy chain or light chain of the antibody or of its portion, an isolated
 CC nucleic acid molecule comprising a nucleotide sequence encoding the heavy
 CC chain or its antigen-binding portion or the light chain or its antigen-
 CC binding portion of an antibody described above, a vector comprising the
 CC nucleic acid molecule, where the vector optionally comprises an
 CC expression control sequence operably linked to the nucleic acid molecule,
 CC a host cell comprising the vector or the nucleic acid molecule above, a
 CC method of producing a human monoclonal antibody or its antigen-binding
 CC portion that specifically binds MAdCAM, a method of isolating an antibody
 CC or its antigen-binding portion that specifically binds to MAdCAM, a
 CC method of treating a subject in need of a human antibody or its antigen-
 CC binding portion that specifically binds to MAdCAM and inhibits binding to
 CC alpha4beta7, a method of inhibiting alpha4beta7 binding to cells
 CC expressing human MAdCAM, a method of inhibiting MAdCAM-mediated leukocyte
 CC -endothelial cell adhesion, migration and infiltration into tissues, a
 CC method of inhibiting alpha4beta7/MAdCAM-dependent cellular adhesion,
 CC inhibiting the MAdCAM-mediated recruitment of lymphocytes to
 CC gastrointestinal lymphoid tissue, a method of diagnosing a disorder
 CC characterized by circulating soluble human MAdCAM and detecting
 CC inflammation in a subject. The antibody, composition and methods are
 CC useful for diagnosing and treating inflammatory disease, e.g.,
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
 CC diverticular disease, gastritis, liver disease, primary biliary
 CC cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and
 CC graft versus host disease. This sequence represents a human monoclonal
 CC anti-MAdCAM antibody related protein of the invention.

XX Sequence 122 AA;

Query Match 80.0%; Score 48; DB 9; Length 122;

Best Local Similarity 63.6%; Pred. No. 2.5;

Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LATYYFGLDV 11

DB 100 VVITYYGMVDV 110

RESULT 4

ADD28082 standard; protein; 114 AA.

AC ADD28082;

DT 15-JAN-2004 (first entry)

DB Lymphoma related immunoglobulin variable region.

XX B-cell; malignant; immunoglobulin; immunoglobulin variable region;
 KW Ig variable region; glycosylation site; lymphoma; B cell receptor;
 KW cytoskeletal; gene therapy; glycosylation inhibitor;
 KW non-Hodgkin's lymphoma.

OS Synthetic.

OS Homo sapiens.

PN WO2003074059-A2.

PD 12-SEP-2003.

PF 24-FEB-2003; 2003WO-GB000783.

PR 07-MAR-2002; 2002GB-00005395.

XX (CAN-C) CANCER RES TECHNOLOGY LTD.

PI Zhu D, Stevenson F;

DR WPI; 2003-902720/82.

PT Classifying a B-cell as malignant or normal by isolating a sequence
 PT representing an Ig variable region from the B cell, detecting the
 PT presence of a glycosylation site and classifying the cell as malignant or
 PT normal.

PS Disclosure; Fig 3; 61pp; English.

XX The present invention describes a method for classifying a B-cell as
 CC malignant or normal comprising: (a) isolating a sequence representing an
 CC immunoglobulin (Ig) variable region from the B cell; (b) detecting the
 CC presence of a glycosylation site; and (c) classifying the cell as
 CC malignant or normal on the basis of the presence or absence of a
 CC glycosylation site. Also described: (1) treating a patient suffering from
 CC or at risk of having lymphoma; (2) screening for substances capable of
 CC inhibiting glycosylation of the Ig variable region of the B cell receptor
 CC ; and (3) screening for substances (S) capable of inhibiting the
 CC interaction between lectins of the type found in the germinal centre and
 CC N-glycans found on the surface of Ig of lymphoma cells. (S) has
 CC cytototoxic activity, and can be used in gene therapy, and as a
 CC glycosylation inhibitor. The method is useful in classifying a B-cell as
 CC malignant or normal. The glycosylation inhibitor is useful in preparing a
 CC medicament for treating non-Hodgkin's lymphoma. The present sequence
 CC represents an Ig variable region sequence which is used in the
 CC exemplification of the present invention.

SO Sequence 114 AA;

Query Match 78.3%; Score 47; DB 7; Length 114;

Best Local Similarity 77.8%; Pred. No. 3.4;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 TYYFGLDV 11

DB 106 TYYFGMDV 114

RESULT 5

ADD28323 standard; protein; 129 AA.

AC ADD28323;

DT 15-JAN-2004 (first entry)

DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:101.

XX human heterodimeric antibody; human; antibody; binding affinity;
 KW protective antigen; Bacillus anthracis; anthrax infection; cell receptor;
 KW edema factor; lethal factor; virulence; antibacterial; immunotherapy;
 KW anti-toxin; anti-infective; anthrax; botulinum; smallpox;
 KW Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.

OS Synthetic.

OS Homo sapiens.

PN WO2003076568-A2.

PD 18-SEP-2003.

PF 11-FEB-2003; 2003WO-US004206.

PR 11-FEB-2002; 2002US-0356086P.

PR 29-APR-2002; 2002US-0376408P.

PR 27-SEP-2002; 2002US-0414053P.

PR 25-NOV-2002; 2002US-0428807P.

PA (ALEX-) ALEXION PHARM INC.
XX Bowdish KS, Wild MA;
XX WPI; 2003-722327/68.
XX
XX New human heterodimeric antibodies or their antibody fragments, useful as
PT anti-toxins or anti-infectives with respect to infective agents, e.g.
PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West
PT Nile virus.
XX
XX Claim 11; SEQ ID NO 101; 67pp; English.
XX
XX The present invention describes a human heterodimeric antibody (I)
CC (fragment) having a binding affinity of at least 1x10⁻⁸ M to the
CC protective antigen of Bacillus anthracis or a molecule involved in
CC anthrax infection that blocks binding of the antigen or molecule to cell
CC receptors, edema factor and lethal factor. (I) has virucide and
CC antibacterial activities, and can be used in immunotherapy. The
CC antibodies (I) are useful as anti-toxins or anti-infectives with respect
CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan
CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The
CC present sequence represents a human heterodimeric antibody heavy chain
CC variable region amino acid sequence, which is used in the exemplification
CC of the present invention.
XX
SQ Sequence 129 AA;
Query Match 78.3%; Score 47; DB 7; Length 129;
Best Local Similarity 77.8%; Pred. No. 3.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 3 TYYYFGLDV 11
|||:|:
Db 105 TYYYGMDV 113
RESULT 6
ADD28237
ID ADD28237 standard; protein; 134 AA.
XX
XX ADD28237;
AC
XX
XX 15-JAN-2004 (first entry)
DT
XX
XX Human heterodimeric antibody heavy chain variable region SEQ ID NO:15.
DE
XX
XX human heterodimeric antibody; human; antibody; binding affinity;
KM protective antigen; Bacillus anthracis; anthrax infection; cell receptor;
KM edema factor; lethal factor; virucide; antibacterial; immunotherapy;
KW anti-toxin; anti-infective; anthrax; botulinum; smallpox;
KM Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.
XX
XX Synthetic.
OS
XX Homo sapiens.
PA
XX WO2003076568-A2.
PN
XX
XX 18-SEP-2003.
PD
XX
XX 11-FEB-2003; 2003WO-US004206.
PF
XX
XX 11-FEB-2002; 2002US-0356086P.
PR
XX 29-APR-2002; 2002US-0376408P.
PR
XX 27-SEP-2002; 2002US-0414053P.
PR
XX 25-NOV-2002; 2002US-0428807P.
XX
XX (ALEX-) ALEXION PHARM INC.
PA
XX Bowdish KS, Wild MA;
PI
XX WPI; 2003-722327/68.
DR
XX

PT New human heterodimeric antibodies or their antibody fragments, useful as
PT anti-toxins or anti-infectives with respect to infective agents, e.g.
PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West
PT Nile virus.
XX
XX Claim 6; SEQ ID NO 15; 67pp; English.
XX
XX The present invention describes a human heterodimeric antibody (I)
CC (fragment) having a binding affinity of at least 1x10⁻⁸ M to the
CC protective antigen of Bacillus anthracis or a molecule involved in
CC anthrax infection that blocks binding of the antigen or molecule to cell
CC receptors, edema factor and lethal factor. (I) has virucide and
CC antibacterial activities, and can be used in immunotherapy. The
CC antibodies (I) are useful as anti-toxins or anti-infectives with respect
CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan
CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The
CC present sequence represents a human heterodimeric antibody heavy chain
CC variable region amino acid sequence, which is used in the exemplification
CC of the present invention.
XX
SQ Sequence 134 AA;
Query Match 78.3%; Score 47; DB 7; Length 134;
Best Local Similarity 77.8%; Pred. No. 4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 3 TYYYFGLDV 11
|||:|:
Db 110 TYYYGMDV 118
RESULT 7
ADV86824
ID ADV86824 standard; protein; 134 AA.
XX
XX ADV86824;
AC
XX
XX 10-MAR-2005 (first entry)
DT
XX
XX Bacillus anthracis toxin Fab 9 K 2e G pro heavy chain variable region.
DE
XX
XX Bioreactorism; Bacillus anthracis infection; vaccine; diagnosis;
KM antibacterial; antibody; heavy chain variable region.
XX
XX Homo sapiens.
OS
XX
XX WO2004110362-A2.
PN
XX
XX 23-DEC-2004.
PD
XX
XX 26-MAY-2004; 2004WO-US016557.
PF
XX
XX 02-JUN-2003; 2003US-00452593.
XX
XX (ALEX-) ALEXION PHARM INC.
PA
XX Bowdish KS, Frederickson S, Wild MA, Maruyama T, Nolan MJ;
PI
XX WPI; 2005-057715/06.
DR
XX
XX Treating an animal with anthrax infection by administering an antibody to
PT the protective antigen of Bacillus anthracis, and blocking binding to
PT cell receptors, edema factor or lethal factor.
XX
XX Claim 7; SEQ ID NO 15; 67pp; English.
XX
XX A claimed method for treating an animal infected with Bacillus anthracis
CC comprises administering an antibody or antibody fragment that binds to a
CC molecule involved in anthrax infection and which has the ability to block
CC the binding of the molecule to at least one of a cell receptor, PA63,
CC PA63 heptamer, PA83, edema factor and lethal factor. A claimed method for
CC determining exposure to B. anthracis comprises assaying a sample for the
CC presence of a molecule selected from cell receptors, PA63, PA63 heptamer,

PA63, edema factor or lethal factor with an antibody that has binding affinity for the molecule, where the presence of elevated levels of the antibody correlates with the presence of a disease associated with B. anthracis. Alternatively, the method involves assaying for the presence of an antibody to a cell receptor, PA63, PA63 heptamer, PA63, edema factor or lethal factor with a secondary antibody having binding affinity for the antibody, where the presence of elevated levels of the secondary antibody correlates with the presence of B. anthracis in a subject. In all cases, the antibody (full-length or functional fragment) may comprise a heavy chain variable region selected from a group of sequences ADV86810-ADV86827, a light chain kappa region selected from a group of sequences ADV86828-ADV86835 and a light chain lambda region selected from a group of sequences ADV86836-ADV86847. Diagnostic kits are provided. A claimed vaccine comprises a multimer of anthrax toxin PA63. The methods and compositions of the present invention are also useful for producing anti-toxins or anti-infectives to infective agents such as anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis and West Nile virus. The present sequence is that of the heavy chain variable region of a human Fab (designated 9 K 2e G pro) with positive reactivity to anthrax proteins PA63 and PA83. Phage libraries were developed from mRNA isolated from blood and bone marrow samples of donors who had been vaccinated against anthrax. The libraries were panned against PA63 and PA63, and sequence analysis was performed on positive responders. Neutralization of anthrax toxin activity by purified Fabs was demonstrated.

Sequence 134 AA;

Query Match 78.3%; Score 47; DB 9; Length 134;
Best Local Similarity 77.8%; Pred. No. 4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TYYYFGLDV 11
| | | | : | | |
Db 110 TYYYGMDV 118

RESULT 8
ADR28082
ID ADR28082 standard; protein; 244 AA.

XX ADR28082;

DT 07-OCT-2004 (first entry)

XX NPB polypeptide scFv27, seq id 29.

XX Cytostatic; metastasis inhibitor; neuropilin binder; NPB, scFv;
KW single chain antibody; neuropilin-1; NP-1; angiogenesis; tumour; cancer.

XX Mus sp.
OS Synthetic.

XX Key Location/Qualifiers
FH Region 87..103
FT /note="complementary determining region claimed under
claim 5"

XX WO2004056874-A2.

XX 08-JUL-2004.

XX 22-DEC-2003; 2003WO-BP014756.

XX 20-DEC-2002; 2002US-0435893P.

XX 15-JAN-2003; 2003EP-00000615.

XX (XERI-) XERION PHARM AG.

XX (TUFT) UNIV TUFTS.

XX Unger CM, Beate G, Zehetmeier C, Lain B, Torella C, Niswöhner J;
PI Jay DG, Eustace BK, Krauer R, Jensen KH;
XX WPI, 2004-507700/48.

DR N-PSDB; ADR28116.

XX Novel neuropilin binder which is scFv, antibody fragment or bioconjugate,
PT that modulates neuropilin-1 function or inhibits NP-1 dependent
PT angiogenesis of endothelial cells and/or invasion of tumor cells useful
PT for treating cancer.

XX Claim 3; SEQ ID NO 29; 120pp; English.

XX The invention relates to a neuropilin binder (NPB) (I) which is a
CC polypeptide, antibody, scFv, antibody fragment or bioconjugate, that
CC modulates neuropilin-1 (NP-1) function or inhibits NP-1 dependent
CC angiogenesis of endothelial cells and/or invasion of tumor cells,
CC whereby the NPB binds to NP-1 and modulates NP-1 function. Further
CC disclosed is an ex vivo method of determining the dependency of the
CC invasiveness of a naturally occurring invasive cancer cell on the
CC functionality of NP-1. The NPB of the invention is an inhibitor of
CC metastasis of NP-1 mediated invasion and/or adhesion and an inhibitor of
CC tumour-associated NP-1 dependent angiogenesis. The NPB of the invention
CC is useful for detecting NP-1 expression, modulation of NP-1 function,
CC particularly modulation or inhibition of NP-dependent invasion or
CC adhesion of cells, preferably tumour cells. It is useful in the
CC manufacture of medicament for the treatment or prevention of NP-dependent
CC angiogenesis and non-physiological blood vessel growth, particularly
CC correlated with a tumour. It is also useful for treatment or prevention
CC of cancer and/or metastasis of tumour cells. The current sequence
CC represents a single chain antibody neuropilin binder (NPB) polypeptide.

Sequence 244 AA;

Query Match 78.3%; Score 47; DB 8; Length 244;
Best Local Similarity 77.8%; Pred. No. 7.7;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TYYYFGLDV 11
| | | | : | | |
Db 95 TYYYGMDV 103

RESULT 9
AEB45891
ID AEB45891 standard; protein; 468 AA.

XX AEB45891;

DT 06-OCT-2005 (first entry)

XX Human monoclonal anti-MAdCAM antibody #27.

XX Monoclonal antibody; mucosal addressin cell adhesion molecule; MAdCAM;
KW inflammation; inflammatory bowel disease; Crohns disease;
KW ulcerative colitis; diverticular disease; gastritis; liver disease;
KW primary biliary cirrhosis; primary sclerosing cholangitis;
KW insulin dependent diabetes; graft versus host disease; antiinflammatory;
KW gastrointestinal-gen.; antitumor; hepatotropic; antidiabetic;
KW immunosuppressive; antibody.

XX Homo sapiens.

XX WO2005067620-A2.

XX 28-JUL-2005.

XX 07-JAN-2005; 2005WO-US000370.

XX 09-JAN-2004; 2004US-0535490P.

XX (PRIZ) PRIZER INC.

XX (ABGE-) ABGENIX INC.

XX (PRIZ) PRIZER LTD.

XX Pullen N, Molloy E, Kellermann S, Green LT, Haak-Frendocho M;
XX

DR WPI: 2005-554958/56.
 DR N-PSDB; AEB45890.
 XX
 XX New antibody to Mucosal Adressin Cell Adhesion Molecule, useful for
 PT diagnosing and treating an inflammatory disease, e.g. inflammatory bowel
 PT disease, ulcerative colitis, gastritis, insulin-dependent diabetes or
 PT graft versus host disease.
 XX
 XX Claim 8; SEQ ID NO 56; 167bp; English.
 PS
 XX The invention relates to a human monoclonal antibody or its antigen-
 CC binding portion that specifically binds to mucosal adressin cell
 CC adhesion molecule (MAdCAM). The invention also relates to a hybridoma
 CC cell line that produces the human monoclonal antibody, a pharmaceutical
 CC composition comprising an amount of the monoclonal antibody or its
 CC antigen-binding portion and a pharmaceutical carrier, a method of
 CC treating inflammatory disease in a subject, an isolated cell line that
 CC produces the monoclonal antibody or its antigen-binding portion or the
 CC heavy chain or light chain of the antibody or of its portion, an isolated
 CC nucleic acid molecule comprising a nucleotide sequence encoding the heavy
 CC chain or its antigen-binding portion or the light chain or its antigen-
 CC binding portion of an antibody described above, a vector comprising the
 CC nucleic acid molecule, where the vector optionally comprises an
 CC expression control sequence operably linked to the nucleic acid molecule,
 CC a host cell comprising the vector or the nucleic acid molecule above, a
 CC method of producing a human monoclonal antibody or its antigen-binding
 CC portion that specifically binds MAdCAM, a method of isolating an antibody
 CC or its antigen-binding portion that specifically binds to MAdCAM, a
 CC method of treating a subject in need of a human antibody or its antigen-
 CC binding portion that specifically binds to MAdCAM and inhibits binding to
 CC alpha-beta7, a method of inhibiting alpha-beta7 binding to cells
 CC expressing human MAdCAM, a method of inhibiting MAdCAM-mediated leukocyte
 CC -endothelial cell adhesion, migration and infiltration into tissues, a
 CC method of inhibiting alpha-beta7/MAdCAM-dependent cellular adhesion,
 CC inhibiting the MAdCAM-mediated recruitment of lymphocytes to
 CC gastrointestinal lymphoid tissue, a method of diagnosing a disorder
 CC characterized by circulating soluble human MAdCAM and detecting
 CC inflammation in a subject. The antibody, composition and methods are
 CC useful for diagnosing and treating inflammatory disease, e.g.
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
 CC diverticular disease, gastritis, liver disease, primary biliary
 CC cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and
 CC graft versus host disease. This sequence represents a human monoclonal
 CC anti-MAdCAM antibody of the invention.
 CC
 XX
 XX Sequence 468 AA;
 SQ
 Query Match 78.3%; Score 47; DB 9; Length 468;
 Best Local Similarity 77.8%; Pred. No. 15;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 3 TTYVFGLDV 11
 |||||:
 Db 123 TTYVYGMVDV 131
 RESULT 10
 AEB45853
 ID AEB45853 standard; protein; 469 AA.
 XX
 AC AEB45853;
 XX
 DT 06-OCT-2005 (first entry)
 XX
 XX Human monoclonal anti-MAdCAM antibody #9.
 DE
 XX Monoclonal antibody; mucosal adressin cell adhesion molecule; MAdCAM;
 KM inflammation; inflammatory bowel disease; Crohn's disease;
 KM ulcerative colitis; diverticular disease; gastritis; liver disease;
 KM primary biliary cirrhosis; primary sclerosing cholangitis;
 KM insulin dependent diabetes; graft versus host disease; anti-inflammatory;
 KM gastrointestinal gen.; antiulcer; hepatotropic; antidiabetic;
 KM immunosuppressive; antibody.

XX
 OS Homo sapiens.
 XX
 XX WO2005067620-A2.
 FN
 XX 28-JUL-2005.
 PD
 XX
 XX 07-JAN-2005; 2005WO-US000370.
 PF
 XX 09-JAN-2004; 2004US-0535490P.
 PR
 XX (PRIZ) PRIZER INC.
 PA (ABGE-) ABGENIX INC.
 PA (PRIZ) PRIZER LTD.
 XX
 P1 Pullen N, Molloy E, Kellermann S, Green LL, Haak-Frendelcho M;
 XX
 XX WPI: 2005-554958/56.
 DR N-PSDB; AEB45852.
 DR
 XX
 XX New antibody to Mucosal Adressin Cell Adhesion Molecule, useful for
 PT diagnosing and treating an inflammatory disease, e.g. inflammatory bowel
 PT disease, ulcerative colitis, gastritis, insulin-dependent diabetes or
 PT graft versus host disease.
 XX
 XX Claim 8; SEQ ID NO 18; 167bp; English.
 PS
 XX The invention relates to a human monoclonal antibody or its antigen-
 CC binding portion that specifically binds to mucosal adressin cell
 CC adhesion molecule (MAdCAM). The invention also relates to a hybridoma
 CC cell line that produces the human monoclonal antibody, a pharmaceutical
 CC composition comprising an amount of the monoclonal antibody or its
 CC antigen-binding portion and a pharmaceutical carrier, a method of
 CC treating inflammatory disease in a subject, an isolated cell line that
 CC produces the monoclonal antibody or its antigen-binding portion or the
 CC heavy chain or light chain of the antibody or of its portion, an isolated
 CC nucleic acid molecule comprising a nucleotide sequence encoding the heavy
 CC chain or its antigen-binding portion or the light chain or its antigen-
 CC binding portion of an antibody described above, a vector comprising the
 CC nucleic acid molecule, where the vector optionally comprises an
 CC expression control sequence operably linked to the nucleic acid molecule,
 CC a host cell comprising the vector or the nucleic acid molecule above, a
 CC method of producing a human monoclonal antibody or its antigen-binding
 CC portion that specifically binds MAdCAM, a method of isolating an antibody
 CC or its antigen-binding portion that specifically binds to MAdCAM, a
 CC method of treating a subject in need of a human antibody or its antigen-
 CC binding portion that specifically binds to MAdCAM and inhibits binding to
 CC alpha-beta7, a method of inhibiting alpha-beta7 binding to cells
 CC expressing human MAdCAM, a method of inhibiting MAdCAM-mediated leukocyte
 CC -endothelial cell adhesion, migration and infiltration into tissues, a
 CC method of inhibiting alpha-beta7/MAdCAM-dependent cellular adhesion,
 CC inhibiting the MAdCAM-mediated recruitment of lymphocytes to
 CC gastrointestinal lymphoid tissue, a method of diagnosing a disorder
 CC characterized by circulating soluble human MAdCAM and detecting
 CC inflammation in a subject. The antibody, composition and methods are
 CC useful for diagnosing and treating inflammatory disease, e.g.
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
 CC diverticular disease, gastritis, liver disease, primary biliary
 CC cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and
 CC graft versus host disease. This sequence represents a human monoclonal
 CC anti-MAdCAM antibody of the invention.
 CC
 XX
 XX Sequence 469 AA;
 SQ
 Query Match 78.3%; Score 47; DB 9; Length 469;
 Best Local Similarity 77.8%; Pred. No. 15;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 3 TTYVFGLDV 11
 |||||:
 Db 123 TTYVYGMVDV 131

RESULT 11
ID ADR38712 standard; peptide; 13 AA.
XX ADR38712;
XX
XX
XX 02-DEC-2004 (first entry)
XX
XX Mouse heavy chain variable region CDR3 seqid 114.
DE
XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
XX BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
XX toxin neutralisation; botulinum neurotoxin poisoning; mouse;
XX heavy chain variable region; complementarity determining region; CDR3.
XX
XX Mus sp.
XX
XX US2004175385-A1.
XX
XX 09-SEP-2004.
XX
XX 01-AUG-2003; 2003US-00632706.
XX
XX 31-AUG-1998; 98US-00144886.
XX 01-AUG-2002; 2002US-0400721P.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Marks JD, Amersdorfer P;
XX
XX WPI; 2004-652009/63.
XX
XX New isolated antibody that neutralizes botulinum neurotoxin type A,
PT useful for diagnosing botulism or for treating pathologies associated
PT with botulinum neurotoxin poisoning.
XX
XX Example 3; SEQ ID NO 114; 110pp; English.
XX
XX The invention describes an isolated antibody (I) that specifically binds
XX to an epitope specifically bound by an antibody expressed by a specific
XX clone where (I) binds to and neutralises botulinum neurotoxin type A
XX (BONT/A). An isolated antibody (I) that specifically binds to an epitope
XX specifically bound by an antibody expressed by a clone chosen from clone
XX S25, C25, C39, 1C6, 3D12, B4, 1P3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
XX 3-8, 3-10 and 1NK1, where (I) binds to and neutralizes botulinum
XX neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
XX comprising BONT/A neutralising epitope having an epitope that is
XX specifically bound by an antibody expressed by clones as mentioned in (I)
XX ; producing (I); and a composition (III) comprising several anti-
XX botulinum neurotoxin antibodies, where each antibody is specific for a
XX different epitope of a botulinum neurotoxin and the combination of
XX antibodies shows greater toxin neutralisation than the single antibodies
XX in surplus. The following are disclosed: a pharmaceutical composition
XX comprising (I); and a kit comprising (I). (I) is useful for neutralising
XX BONT/A antibody and for neutralising a botulinum neurotoxin which
XX involves contacting neurotoxin with (I) in surplus, where each of (I) is
XX specific for a different epitope of the botulinum neurotoxin and the
XX combination of antibodies shows greater toxin neutralisation than the
XX single antibodies in surplus. (I) is useful for diagnosing the botulism
XX or for treating pathologies associated with botulinum neurotoxin
XX poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
XX enables rapid detection or diagnosis of botulism. This is the amino acid
XX sequence of mouse heavy chain variable region complementarity determining
XX region 3 (CDR3) from anti-botulinum neurotoxin antibodies.
XX
XX Sequence 13 AA;
SQ

Query Match 76.7%; Score 46; DB 8; Length 13;
Best Local Similarity 70.0%; Pred. No. 0.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 ATYYFGGLDV 11
| | | | | | | | | | | | | | |

Db 4 ANYYYGMGV 13
RESULT 12
ID ADW04816 standard; peptide; 21 AA.
XX ADW04816;
XX
XX
XX 07-APR-2005 (first entry)
XX
XX PAPP-A immunoglobulin variable domain AB b03 heavy chain CDR3 SEQ ID 141.
DE
XX Cysteatic; Vasotropic; heavy chain variable domain;
XX proliferative disorder; restenosis; glioblastoma; osteosarcoma.
XX
XX Unidentified.
XX
XX OS
XX US2005009136-A1.
XX
XX PN 13-JAN-2005.
XX
XX PD 19-FEB-2004; 2004US-00783311.
XX
XX PE 19-FEB-2003; 2003US-0448515P.
XX
XX PR 19-FEB-2003; 2003US-0448515P.
XX
XX PA (DYAX-) DYAX CORP.
XX
XX P1 Nixon A, Hogan S;
XX
XX P1
XX WPI; 2005-080519/09.
XX
XX New pregnancy-associated plasma protein-A (PAPP-A) binding proteins
PT comprising immunoglobulin variable domain sequences, useful for
PT diagnosing, preventing or treating diseases such as cancer.
XX
XX Example; SEQ ID NO 141; 168pp; English.
XX
XX The present invention relates to novel proteins (I) that bind to
XX pregnancy-associated plasma protein A (PAPP-A ADW04676). (I) comprises a
XX first and second immunoglobulin variable domain sequence which binds to
XX PAPP-A. Also claimed are proteins (II) which comprise light chain (LC)
XX and heavy chain immunoglobulin variable domain sequences which binds to
XX PAPP-A. The proteins are useful for diagnosing, preventing or treating
XX proliferative diseases such as glioblastoma, osteosarcoma and overgrowth
XX of vascular smooth muscle cells following e.g., balloon angioplasty
XX (which may cause restenosis). The proteins are especially useful for
XX useful for treating diseases involving IGF regulated growth. The present
XX sequence is one such immunoglobulin variable domain sequence.
XX
XX Sequence 21 AA;
SQ

Query Match 76.7%; Score 46; DB 9; Length 21;
Best Local Similarity 63.6%; Pred. No. 0.83;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 LATYYFGGLDV 11
| | | | | | | | | | | | | | |
Db 11 LGNYYYGMGV 21
| | | | | | | | | | | | | | |
RESULT 13
ID ADZ41994 standard; peptide; 126 AA.
XX ADZ41994;
XX
XX AC ADZ41994;
XX
XX 30-JUN-2005 (first entry)
XX
XX DT Ig H chain variable region, B-CLL set II peptide #4.
XX
XX DE
XX
XX Antibody; antibody engineering; antibody therapy;
XX light chain variable region; heavy chain variable region;
KW

KM chronic lymphocytic leukemia; cytostatic; Hodgkins disease; lymphoma;
 KM Burkitts lymphoma; multiple myeloma; systemic lupus erythematosus;
 KM antinflammatory; dermatologic; immunosuppressive; myasthenia gravis;
 KM muscular-gen.; neuroproctive; Graves disease; antidiyroid;
 KM insulin dependent diabetes; diabetes mellitus; antidiabetic;
 KM autoimmune hemolytic anemia; antenemic.
 KM
 OS Homo sapiens.
 PN WO2005034733-A2.
 XX
 XX 21-APR-2005.
 PD
 XX 08-OCT-2004; 2004WO-US033176.
 PF
 XX 08-OCT-2003; 2003US-0509473P.
 PR
 XX (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
 PA
 XX Mesemer BT, Chiorazzi N, Albesiano E;
 PI
 XX WPI; 2005-306220/31.
 DR
 XX
 PT New isolated and purified preparation of light chain and heavy chain
 PT antibody genes, useful for diagnosing, preventing or treating B cell
 PT chronic lymphocytic leukemia, or in screening for agents that may treat
 PT such disease.
 PS
 XX Disclosure; Fig 2; 58pp; English.
 XX
 CC The new invention relates to combinations of light chain antibody genes
 CC and heavy chain antibody genes, useful for treating B cell chronic
 CC lymphocytic leukemia (B-CLL). B-CLL is a disease of slowly proliferating
 CC CD5+ B lymphocytes. These cells express low levels of surface membrane Ig
 CC that serves as the receptor for antigen (BCR). Analysis of V region gene
 CC cassette usage has shown that distribution of variable region gene
 CC cassettes used by B-CLL clones differs from that in normal cells, with an
 CC increased frequency of VH3-07, VH4-34, and VH1-69 genes. This implies
 CC that the structure of the antibody molecule, and antigen specificity,
 CC play a role in the leukemic transformation of particular B cells. The
 CC present invention discloses that a significant proportion of B-CLL
 CC patients with aggressive disease share the same classes of VH, D, JH, VL
 CC and JH antibody genes, forming sets of patients with highly homologous B
 CC cell receptor. Alternatively, the patients have a disorder selected from
 CC Hodgkin's disease, non-Hodgkin's lymphoma, Burkitt's lymphoma, myeloma or
 CC systemic lupus erythematosus, myasthenia gravis, Grave's disease, type I
 CC diabetes mellitus, autoimmune peripheral neuropathy, and autoimmune
 CC hemolytic anemia. The new members of the antibody genes are: VH4-39/D6-
 CC 13/JH5/VLkappa012/2/JLkappa1/kappa2 (Set I); VH4-34/D5-
 CC 5/JH6/VLkappa017/JLkappa1/kappa2 (Set II); VH3-
 CC 21/JH6/VLlambda03/JLlambda3 (Set III); VH1-69/D3-
 CC 16/JH3/VLkappa027/JLkappa1/kappa4 (Set IV); VH1-69/D3-
 CC 10/JH6/VLlambda03/JLlambda1 (Set V); VH1-02/D6-
 CC 19/JH4/VLkappa012/2/JLkappa1/kappa2 (Set VIA); VH1-03/D6-
 CC 19/JH4/VLkappa012/2/JLkappa1/kappa2 (Set VIB); VH1-18/D6-
 CC 51/D6-19/JH4/VLkappa012/2/JLkappa2 (Set VIC); VH1-46/D6-19/JH4 (Set VID); VH5-
 CC 3/JH4/VLkappa019/JLkappa4 (Set VII); and VH1-69/D3-
 CC 2/JH6/VLkappa067/JLkappa3 (Set VIII). Treating a patient having B-CLL
 CC with the above genes comprises administering an agent that binds to the
 CC antigen-binding region of an antibody encoded by the antibody genes. The
 CC agent is an anti-idiotypic antibody, a peptide antigen, or an aptamer. The
 CC present sequence is an Ig H chain variable region, B-CLL set II peptide.
 CC
 XX
 SQ Sequence 126 AA;
 Query Match 76.7%; Score 46; DB 9; Length 126;
 Best Local Similarity 72.7%; Pred. No. 5.6;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 14
 ADM04810
 ID ADM04810 standard; protein, 140 AA.
 XX
 AC ADM04810;
 XX
 DT 07-APR-2005 (first entry)
 XX
 DE PAPP-A immunoglobulin variable domain AB b03 heavy chain SEQ ID 135.
 XX
 KM Cytostatic; Vascotropic; heavy chain variable domain;
 KM proliferative disorder; restenosis; glioblastoma; osteosarcoma.
 XX
 OS unidentified.
 PN US2005009136-A1.
 XX
 PD 13-JAN-2005.
 PF 19-FEB-2004; 2004US-00783311.
 PR 19-FEB-2003; 2003US-0448515P.
 PA (DYAX-) DYAX CORP.
 XX
 PI Nixon A, Hogan S;
 DR WPI; 2005-080519/09.
 XX
 PT New pregnancy-associated plasma protein-A (PAPP-A) binding proteins
 PT comprising immunoglobulin variable domain sequences, useful for
 PT diagnosing, preventing or treating diseases such as cancer.
 PS
 XX Example; SEQ ID NO 135; 168pp; English.
 XX
 CC The present invention relates to novel proteins (I) that bind to
 CC pregnancy-associated plasma protein A (PAPP-A ADM04676). (I) comprises a
 CC first and second immunoglobulin variable domain sequence which binds to
 CC PAPP-A. Also claimed are proteins (II) which comprise light chain (LC)
 CC and heavy chain immunoglobulin variable domain sequences which binds to
 CC PAPP-A. The proteins are useful for diagnosing, preventing or treating
 CC proliferative diseases such as glioblastoma, osteosarcoma and overgrowth
 CC of vascular smooth muscle cells following e.g., balloon angioplasty
 CC (which may cause restenosis). The proteins are especially useful for
 CC useful for treating diseases involving IGF regulated growth. The present
 CC sequence is one such immunoglobulin variable domain sequence.
 CC
 XX
 SQ Sequence 140 AA;
 Query Match 76.7%; Score 46; DB 9; Length 140;
 Best Local Similarity 63.6%; Pred. No. 6.3;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LATYYFGLDV 11
 | | | | | | | |
 DB 109 LGNYYGYMDV 119

RESULT 15
 ADM04952
 ID ADM04952 standard; peptide, 16 AA.
 XX
 AC ADM04952;
 XX
 DT 07-APR-2005 (first entry)
 XX
 DE PAPP-A immunoglobulin variable domain AB f03 heavy chain CDR3 SEQ ID 277.
 XX
 KM Cytostatic; Vascotropic; heavy chain variable domain;
 KM proliferative disorder; restenosis; glioblastoma; osteosarcoma.
 XX

OS Unidentified.

XX US2005009136-A1.

XX 13-JAN-2005.

XX 19-FEB-2004; 2004US-00783311.

XX 19-FEB-2003; 2003US-0448515P.

XX (DYAX-) DYAX CORP.

XX Nixon A, Hogan S;

XX WPI, 2005-080519/09.

PT New pregnancy-associated plasma protein-A (PAPP-A) binding proteins
 PT comprising immunoglobulin variable domain sequences, useful for
 PT diagnosing, preventing or treating diseases such as cancer.

PS Example; SEQ ID NO 277; 168bp; English.

CC The present invention relates to novel proteins (I) that bind to
 CC pregnancy-associated plasma protein A (PAPP-A ADW04676). (I) comprises a
 CC first and second immunoglobulin variable domain sequence which binds to
 CC PAPP-A. Also claimed are proteins (II) which comprise light chain (LC)
 CC and heavy chain immunoglobulin variable domain sequences which binds to
 CC PAPP-A. The proteins are useful for diagnosing, preventing or treating
 CC proliferative diseases such as glioblastoma, osteosarcoma and overgrowth
 CC of vascular smooth muscle cells following e.g., balloon angioplasty
 CC (which may cause restenosis). The proteins are especially useful for
 CC useful for treating diseases involving IGF regulated growth. The present
 CC sequence is one such immunoglobulin variable domain sequence.

XX Sequence 16 AA;

Query Match 75.0%; Score 45; DB 9; Length 16;
 Best Local Similarity 63.6%; Pred. No. 0.92;

Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LATYYFGLDV 11

Db 6 VAGYYYGMDV 16

Search completed: December 4, 2005, 04:44:54
 Job time : 98.5625 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:45 ; Search time 15.5833 Seconds
(without alignments)
67.918 Million cell updates/sec

Title: US-10-632-706-127
Perfect score: 60
Sequence: 1 LATYYFGLDV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query length	ID	Description
1	43	71.7	19	PH1307	Ig heavy chain DJ
2	43	71.7	23	PH1361	Ig heavy chain DJ
3	43	71.7	29	PH1328	Ig heavy chain DJ
4	43	71.7	160	D70189	conserved hypotetic
5	43	71.7	160	S05271	Ig heavy chain pre
6	43	71.7	408	E70380	Na+/H+-exchanging
7	42	70.0	19	PH1304	Ig heavy chain DJ
8	42	70.0	19	S43960	Ig mu chain V regi
9	42	70.0	23	PH1364	Ig heavy chain DJ
10	42	70.0	24	PT0258	Ig heavy chain CDR
11	42	70.0	27	PH1371	Ig heavy chain DJ
12	42	70.0	27	PH1355	Ig heavy chain DJ
13	42	70.0	74	S25793	Ig heavy chain V r
14	42	70.0	118	PH1666	Ig heavy chain V r
15	42	70.0	119	PH0961	Ig heavy chain V r
16	42	70.0	120	PH1650	Ig heavy chain V r
17	42	70.0	125	S24686	Ig heavy chain V6
18	42	70.0	128	S48797	Ig heavy chain V r
19	42	70.0	132	PH0954	Ig heavy chain V r
20	42	70.0	133	C33548	Ig heavy chain V-1
21	42	70.0	136	A49047	Ig heavy chain V-1
22	42	70.0	147	I37780	Ig variable region
23	42	70.0	627	S14683	Ig mu chain precu
24	40	66.7	22	PH1325	Ig heavy chain DJ
25	39.5	65.8	581	E03729	adenine deaminase
26	39	65.0	126	S44107	Ig heavy chain V-D
27	39	65.0	375	A83788	spore germination
28	38	63.3	22	PH1359	Ig heavy chain DJ
29	38	63.3	45	PL0094	Ig heavy chain V r

30	38	63.3	287	2	T27056	hypothetical prote
31	38	63.3	473	2	H86240	hypothetical prote
32	38	63.3	979	2	A39792	transcription acti
33	37	61.7	14	2	PH1601	Ig H chain V-D-J r
34	37	61.7	126	1	MH100U	Ig heavy chain V-I
35	37	61.7	276	2	S16892	probable transpos
36	37	61.7	447	2	T09809	NADH2 dehydrogen
37	37	61.7	448	2	T12006	glycerol-3-phosph
38	37	61.7	527	2	C70130	conditioned mediu
39	37	61.7	571	2	A42138	conditoned mediu
40	37	61.7	571	2	S24482	se1-1 protein - Ca
41	37	61.7	685	2	T22223	Ig heavy chain V r
42	36.5	60.8	120	2	E49590	hypothetical prote
43	36.5	60.8	316	2	C75205	Ig heavy chain DJ
44	36	60.0	18	2	PH1368	36S ribosomal prot
45	36	60.0	145	2	H97707	

ALIGNMENTS

RESULT 1
PH1307
Ig heavy chain DJ region (clone C96-119) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1307
R:Masserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1307
A:Molecule type: DNA
A:Residues: 1-19 <MAS>
A:Cross-references: UNIPARC:UPI0000176935
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 71.7%; Score 43; DB 2; Length 19;
Best Local Similarity 66.7%; Pred. No. 0.23;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TYYFGLDV 11
Db 6 SYTYGMDV 14

RESULT 2

PH1361
Ig heavy chain DJ region (clone C178-122B) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1361
R:Masserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1361
A:Molecule type: DNA
A:Residues: 1-23 <MAS>
A:Cross-references: UNIPARC:UPI0000176948
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 71.7%; Score 43; DB 2; Length 23;
Best Local Similarity 63.6%; Pred. No. 0.28;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 LATYYFGLDV 11
Db 8 LFPYYGMDV 18

```
RESULT 3
PH1328
Ig heavy chain DJ region (clone C113-148) - human (fragment)
A:Residues: 1-144 <K1S2>
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1328
R:Masserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1328
A:Molecule type: DNA
A:Residues: 1-29 <WAS>
A:Cross-references: UNIPARC:UPI0000176939
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match
Best Local Similarity 71.7%; Score 43; DB 2; Length 29;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYVFGLDV 11
: |||: ||
Db 16 SYTYGMDV 24

RESULT 4
D70189
conserved hypothetical integral membrane protein BB0717 - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: D70189
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kexlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horc, K.; Roberts, K.; Hatch, B.
Nature 330, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: D70189
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-160 <KLB>
A:Cross-references: UNIPROT:O51659; UNIPARC:UPI00000575B2; GB:AE001171; GB:AE000783; NID
A:Experimental source: strain B31

Query Match
Best Local Similarity 71.7%; Score 43; DB 2; Length 160;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATYYFGLDV 11
: |||: ||
Db 23 ATYFYSIDI 32

RESULT 5
S05271
Ig heavy chain precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Dec-2004
C:Accession: S05271; S04602
R:Kishimoto, T.
submitted to the EMBL Data Library, March 1989
A:Reference number: S05270
A:Accession: S05271
A:Molecule type: mRNA
A:Residues: 1-160 <K1S1>
A:Cross-references: UNIPROT:Q96B89; UNIPARC:UPI0000176B50; EMBL:X14584
R:Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
A:Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of
A:Reference number: S04601; MUID:89296497; PMID:250664
A:Accession: S04602
```

```
A:Molecule type: mRNA
A:Residues: 1-144 <K1S2>
A:Cross-references: UNIPARC:UPI0000176B51; EMBL:X14584
C:Superfamily: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F11-19/Domain: signal sequence #status predicted <SIG>
F120-160/Product: Ig heavy chain (fragment) #status predicted <MAT>
F134-117/Domain: immunoglobulin homology <IMW>

Query Match
Best Local Similarity 71.7%; Score 43; DB 2; Length 160;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYVFGLDV 11
: |||: ||
Db 125 SYTYGMDV 133

RESULT 6
E70380
Na+/H+-exchanging protein - Aquifex aeolicus
N:Alternate names: Na+/H+ antiporter
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: E70380
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: E70380
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-408 <AGP>
A:Cross-references: UNIPROT:O67072; UNIPARC:UPI00000564AB; GB:AE000714; NID:G2983446; PI
A:Experimental source: strain VF5
C:Genetics:
A:Gene: napA2
C:Superfamily: Aquifex aeolicus Na+/H+-exchanging protein napA1

Query Match
Best Local Similarity 71.7%; Score 43; DB 2; Length 408;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LATYYFGLDV 11
: |||: ||
Db 116 IVSYFFGLDL 126

RESULT 7
PH1304
Ig heavy chain DJ region (clone C439-111) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1304
R:Masserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1304
A:Molecule type: DNA
A:Residues: 1-19 <WAS>
A:Cross-references: UNIPARC:UPI0000176934
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match
Best Local Similarity 70.0%; Score 42; DB 2; Length 19;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
: |||: ||
Db 7 YYYGMDV 14
```

RESULT 8

S43960
Ig mu chain V region (clone 18) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C:Accession: S43960
R:Wagner, S.D.; Williams, G.T.; Larson, T.; Neuburger, M.S.; Kitamura, D.; Rajewsky, K.;
Nucleic Acids Res. 22, 1389-1393, 1994
A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
A:Reference number: S43956; MUID:94248036; PMID:8190629
A:Accession: S43960
A:Molecule type: DNA
A:Residues: 1-19 <WAS>
A:Cross-references: UNIPARC:UPI000017690D
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 19;
Best Local Similarity 75.0%; Pred. No. 0.35;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
|||:|:|
DB 10 YYYGMDV 17

RESULT 9

PH1364
Ig heavy chain DJ region (clone C178-136A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1364
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1364
A:Molecule type: DNA
A:Residues: 1-23 <WAS>
A:Cross-references: UNIPARC:UPI0000176949
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 23;
Best Local Similarity 75.0%; Pred. No. 0.42;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
|||:|:|
DB 11 YYYGMDV 18

RESULT 10

PT0258
Ig heavy chain CDR3 region (clone 2-118B) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-May-1997
C:Accession: PT0258
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Cacon, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0258
A:Molecule type: DNA
A:Residues: 1-24 <YAM>
A:Cross-references: UNIPARC:UPI0000176940
A:Experimental source: B lymphocyte
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 24;

Best Local Similarity 75.0%; Pred. No. 0.44;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
|||:|:|
DB 12 YYYGMDV 19

RESULT 11

PH1371
Ig heavy chain DJ region (clone C111-145) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1371
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1371
A:Molecule type: DNA
A:Residues: 1-27 <WAS>
A:Cross-references: UNIPARC:UPI000017694B
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 27;
Best Local Similarity 75.0%; Pred. No. 0.5;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
|||:|:|
DB 15 YYYGMDV 22

RESULT 12

PH1355
Ig heavy chain DJ region (clone C100-136) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1355
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1355
A:Molecule type: DNA
A:Residues: 1-27 <WAS>
A:Cross-references: UNIPARC:UPI0000176945
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 27;
Best Local Similarity 75.0%; Pred. No. 0.5;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
|||:|:|
DB 15 YYYGMDV 22

RESULT 13

S26793
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26793
R:Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fami
A:Reference number: S26786; MUID:92111632; PMID:1730251
A:Accession: S26793
A:Status: preliminary
A:Molecule type: mRNA

A,Residues: 1-74 <MOR>
 A,Cross-references: UNIPARC:UPI0000115FCA; EMBL:X61019; NID:G32787; PIDN:CAA43353.1; PID
 C,Superfamily: immunoglobulin V region; immunoglobulin homology
 C,Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 74;
 Best Local Similarity 75.0%; Pred. No. 1.4;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
 |||:|:|
 Db 56 YYYGMDV 63

RESULT 14

PH1666
 Ig heavy chain V region (clone 6C9) - human (fragment)
 C,Species: Homo sapiens (man)
 C,Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
 C,Accession: PH1666
 R,Hillson, J.L.; Karr, N.S.; Opliger, I.R.; Mannik, M.; Sasso, E.H.
 J. Exp. Med. 178, 331-336, 1993
 A,Title: The structural basis of germ-line-encoded VH3 immunoglobulin binding to staphylo
 A,Reference number: PH1642; MUID:93301610; PMID:8315388
 A,Accession: PH1666
 A,Molecule type: mRNA
 A,Residues: 1-118 <HIL>
 A,Cross-references: UNIPARC:UPI0000176BE7
 A,Experimental source: B cell
 C,Superfamily: immunoglobulin V region; immunoglobulin homology
 C,Keywords: heterotetramer; immunoglobulin
 F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 70.0%; Score 42; DB 2; Length 118;
 Best Local Similarity 75.0%; Pred. No. 2.2;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
 |||:|:|
 Db 100 YYYGMDV 107

RESULT 15

PH0961
 Ig heavy chain V region (G6+ T-L33) - human (fragment)
 C,Species: Homo sapiens (man)
 C,Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
 C,Accession: PH0961
 R,Martin, T.; Duffly, S.F.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A,Title: Evidence for somatic selection of natural autoantibodies.
 A,Reference number: PH0952; MUID:92202880; PMID:1552291
 A,Accession: PH0961
 A,Status: nucleic acid sequence not shown
 A,Molecule type: DNA
 A,Residues: 1-119 <MAR>
 A,Cross-references: UNIPARC:UPI0000176CES
 C,Superfamily: immunoglobulin V region; immunoglobulin homology
 C,Keywords: heterotetramer; immunoglobulin
 F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-50/Region: framework 2
 F:51-67/Region: complementarity-determining 2
 F:68-98/Region: framework 3
 F:99-107/Region: complementarity-determining 3

Query Match 70.0%; Score 42; DB 2; Length 119;
 Best Local Similarity 75.0%; Pred. No. 2.2;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
 |||:|:|

Db 101 YYYGMDV 108
 Search completed: December 4, 2005, 04:53:32
 Job time : 17.5833 secs


```
RESULT 2
Q4UFY8_THEAN PRELIMINARY; PRT; 2262 AA.
ID Q4UFY8_THEAN
AC Q4UFY8
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DE Hypoetical protein.
GN ORFNames=TA19710;
OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OX NCBI_TaxID=5874;
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ankara isolate clone C9;
RA Pain A., Renaud H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
RA Hall N., Barrall B.G.,
RT "The chromosome 1 sequence of Theileria annulata."
RL Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR940347; CAI74001.1; -; Genomic_DNA.
KW Hypoetical protein.
SQ
SEQUENCE 2262 AA; 262066 MW; FD9B8915243BF512 CRC64;
Match
Best Local Similarity 73.3%; Score 44; DB 2; Length 2262;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLD 10
Db 1244 STTYFGLD 1251

RESULT 3
OS1659 BORBU PRELIMINARY; PRT; 160 AA.
ID OS1659 BORBU
AC OS1659
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DE 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Conserved hypothetical integral membrane protein.
GN OrderedLocustNames=BB0717;
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
OC Borrelia burgdorferi group.
OX NCBI_TaxID=139;
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685; DOI=10.1038/37551;
RA Frazer C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Latifga R., White O., Ketchum K.A., Dodson R.J., Hickey E.K.,
RA Gwinn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,
RA Richardson D.L., Peterson J.D., Kerlavage A.R., Quackenbush J.,
RA Salzberg S.L., Hanson M., van Vugt R., Palmer N., Adams M.D.,
RA Gocayne J.D., Weidman J.F., Utechtack T.R., Matthey L., McDonald L.A.,
RA Artach P., Bowman C., Garland S.A., Fujii C., Cotton M.D., Horst K.,
RA Roberts K.M., Hatch B., Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochete, Borrelia
burgdorferi."
RL Nature 390:580-586 (1997).
RN EMBL; AE001171; AAC67057.1; -; Genomic_DNA.
DR PIR; D70189; D70189.
DR TIGR; BB0717; -.
KW Complete proteome; Hypoetical protein.
SQ
SEQUENCE 160 AA; 19300 MW; 9DE28A497C0F5737 CRC64;

Query Match
Best Local Similarity 71.7%; Score 43; DB 2; Length 160;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATTYTFFGLDV 11
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Db 23 ATTYTFFSIDI 32

RESULT 4
O660F6 BORBU PRELIMINARY; PRT; 160 AA.
ID O660F6 BORBU
AC O660F6
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DE Conserved hypothetical integral membrane protein.
GN OrderedLocustNames=BB0739;
OS Borrelia garinii.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
OC Borrelia burgdorferi group.
OX NCBI_TaxID=29519;
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PB1;
RA Gloeckner G., Lehmann R., Romualdi A., Pradella S.,
RA Schulte-Spechtel U., Wilske B., Suenkel J., Platzer M.;
RT "Comparative analysis of the Borrelia garinii genome."
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000013; AAU07555.1; -; Genomic_DNA.
KW Complete proteome; Hypoetical protein.
SQ
SEQUENCE 160 AA; 19293 MW; B65B15C5197FB89 CRC64;

Query Match
Best Local Similarity 71.7%; Score 43; DB 2; Length 160;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATTYTFFGLDV 11
Db 23 ATTYTFFSIDI 32

RESULT 5
O67072 AQUAE PRELIMINARY; PRT; 408 AA.
ID O67072 AQUAE
AC O67072
DT 01-AUG-1998 (TRENBLrel. 07, Created)
DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
DE 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Na(+)/H(+) antiporter.
GN Name=napA2; OrderedLocustNames=AQ_929;
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
RA Decker G., Warren P.V., Gaesteland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aulay M., Huber R.,
RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
aeolicus."
RL Nature 392:353-358 (1998).
RN EMBL; AE000714; AAC07034.1; -; Genomic_DNA.
DR PIR; E70380; E70380.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
KW Complete proteome; Transmembrane; Transport.
SQ
SEQUENCE 408 AA; 43582 MW; 7B05B4B387A6C506 CRC64;

Query Match
Best Local Similarity 71.7%; Score 43; DB 2; Length 408;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```


QY 1 LATYFGLDV 11
: : : : :
DB 116 IVSYFFFLDL 126

RESULT 6
QVY71 BORPE PRELIMINARY; PRT; 364 AA.
ID QVY71 BORPE PRELIMINARY; PRT; 364 AA.
AC QVY71 BORPE PRELIMINARY; PRT; 364 AA.
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative periplasmic solute-binding protein.
GN Name=sbmw; OrderedLocustNames=BP1487;
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=520;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Cherevach I.,
RA Achtman M., Atkin R., Baker S., Cronin A., Davis P., Doggett J.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagele K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.,
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640415; CAB41776.1; -; Genomic DNA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006311; Tat.
DR InterPro; IPR004682; TRAP_transpDcTP.
DR Pfam; PF03480; SBP_bac_7; 1.
DR TIGRFAMs; TIGR01405; TAT_signal_seq; 1.
KW Complete proteome.
SQ SEQUENCE 364 AA; 40021 MW; 03F1C2B6F5C1D502 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 364;
Best Local Similarity 77.8%; Pred. No. 38;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATYYFGLD 10
: : : : :
DB 98 ASYYFFGKD 106

RESULT 7
QW926 BORPA PRELIMINARY; PRT; 364 AA.
ID QW926 BORPA PRELIMINARY; PRT; 364 AA.
AC QW926 BORPA PRELIMINARY; PRT; 364 AA.
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative periplasmic solute-binding protein.
GN Name=sbmw; OrderedLocustNames=BP1948;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,

RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagele K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.,
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640428; CAB37248.1; -; Genomic DNA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006311; Tat.
DR InterPro; IPR004682; TRAP_transpDcTP.
DR Pfam; PF03480; SBP_bac_7; 1.
DR TIGRFAMs; TIGR01405; TAT_signal_seq; 1.
KW Complete proteome.
SQ SEQUENCE 364 AA; 39967 MW; 9700BC4608CF1D58 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 364;
Best Local Similarity 77.8%; Pred. No. 38;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATYYFGLD 10
: : : : :
DB 98 ASYYFFGKD 106

RESULT 8
QWKH1 BORBR PRELIMINARY; PRT; 364 AA.
ID QWKH1 BORBR PRELIMINARY; PRT; 364 AA.
AC QWKH1 BORBR PRELIMINARY; PRT; 364 AA.
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative periplasmic solute-binding protein.
GN Name=sbmw; OrderedLocustNames=BB2136;
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagele K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.,
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640443; CAB32632.1; -; Genomic DNA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006311; Tat.
DR InterPro; IPR004682; TRAP_transpDcTP.
DR Pfam; PF03480; SBP_bac_7; 1.
DR TIGRFAMs; TIGR01405; TAT_signal_seq; 1.
KW Complete proteome.
SQ SEQUENCE 364 AA; 39997 MW; 8AB6672BA3BF09AD CRC64;

Query Match 70.0%; Score 42; DB 2; Length 364;
Best Local Similarity 77.8%; Pred. No. 38;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 ATYYFGD 10
 DB 98 ASYYFGKD 106

RESULT 9

Q4QA10 LEIMA
 AC Q4QA10 LEIMA PRELIMINARY; PRT; 378 AA.
 DT 13-SEP-2005 (TRENBLrel. 31, Created)
 DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
 DE Hypothetical protein.
 GN ORFNames=ImjF25_0840;
 OS Leishmania major.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 NC NCB1_TaxID=5664;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=Friedlin;
 RA Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
 RA Smith D., Collins M., Foster N., Harris D., Oliver K., O'Neill S.,
 RA Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CTO05264; CAJ04989.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 378 AA; 41605 MW; 983EB7C7C1F04839 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 378;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TYYFGD 9
 DB 112 TYYFGD 118

RESULT 10

089NT9 BRAJA
 ID 089NT9 BRAJA PRELIMINARY; PRT; 382 AA.
 AC 089NT9;
 DT 01-JUN-2003 (TRENBLrel. 24, Created)
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Periplasmic mannitol-binding protein.
 GN OrderedLocustNames=blc3745;
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 NC NCB1_TaxID=375;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=USDA 110;
 RC MEDLINE=2248498; PubMed=12597275;
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiyama T.,
 RA Sasamoto S., Matsunabe A., Ideasa K., Iriyuchi M., Kawashima K.,
 RA Kohara M., Matsunoto M., Shimo S., Tsuruoka H., Wada T., Yamada M.,
 RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 Bradyrhizobium japonicum USDA110."
 RL DNA Res. 9:189-197(2002).
 DR EMBL; BA000040; BAC49010.1; -; Genomic DNA.
 DR GO; GO:0030288; C:periplasmic space (Genus Gram-negative Bact. .; IBA.
 DR GO; GO:0006810; P:transport; IBA.
 DR InterPro; IPR006311; Tat.
 DR InterPro; IPR004682; TRAP-transpDctP.
 DR Pfam; PF03480; SBP_bac_7.1.
 DR TIGRfam; TIGR01405; TAT_signal_seq; 1.
 KW Complete proteome.
 SQ SEQUENCE 382 AA; 42090 MW; 23C64980A9F98D CRC64;

Query Match 70.0%; Score 42; DB 2; Length 382;
 Best Local Similarity 77.8%; Pred. No. 40;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 ATYYFGD 10
 DB 117 ASYYFGKD 125

RESULT 11

Q7AN07 NANEQ
 ID Q7AN07 NANEQ PRELIMINARY; PRT; 594 AA.
 AC Q7AN07;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE NEQ353.
 GN OrderedLocustNames=NEQ353;
 OS Nanoarchaeum equitans.
 OC Archaea; Nanoarchaeota; Nanoarchaeum.
 NC NCB1_TaxID=160232;
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RP STRAIN=K14-M.
 RC PubMed=1456062; DOI=10.1073/pnas.1735403100;
 RA Waters E., Hohn M.U., Abel I., Graham D.E., Adams M.D., Barnstead M.,
 RA Beeson K.Y., Bibbs L., Bolanos R., Keller M., Kretz K., Lin X.,
 RA Machur E., Ni J., Podar M., Richardson T., Sutton G.G., Simon M.,
 RA Soell D., Stetter K.O., Short J.M., Wooldrifier M.;
 RT "The genome of Nanoarchaeum equitans: insights into early archaeal
 evolution and derived parasitism."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:12984-12988(2003).
 DR EMBL; AE017199; AAR39202.1; -; Genomic_DNA.
 KW Complete proteome.
 SQ SEQUENCE 594 AA; 69673 MW; FD2B60ACF00CD9F4 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 594;
 Best Local Similarity 54.5%; Pred. No. 62;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LATYYFGD 11
 DB 569 LSRHYFGVDI 579

RESULT 12

06GMV2 HUMAN
 ID 06GMV2 HUMAN PRELIMINARY; PRT; 606 AA.
 AC 06GMV2;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE IGHM protein.
 GN Name=IGHM;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Homo.
 NC NCB1_TaxID=9606;
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Primary B-Cells;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Martins A.K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stempleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellier N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Boeck S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huilyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalski U., Smallus D.B.,
RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RU [2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE-Primary B-Cells;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL, BC073758; AAH73758.1; -, mRNA.
DR SMK, Q6GM72; 20-256.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SO SEQUENCE 606 AA; 66185 MW; B6B3B95114E4C55 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 606;
Best Local Similarity 75.0%; Pred. No. 63;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 YYYFGLDV 11
DB 135 YYYFGMDV 142

RESULT 13
O96X97_SULTO PRELIMINARY; PRT; 1062 AA.
AC O96X97;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1062aa long hypothetical thermopain.
GN OrderedLocustNames=ST2615;
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
CC Sulfolobus.
CX NCBI_TaxID=111955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Anai A., Kosugi H., Hosooyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7.";
RL DNA Res. 8:123-140(2001).
DR EMBL, BA000023; BAB67731.1; -, Genomic_DNA.
DR InterPro; IPR007981; Peptidase_A5.
DR Pfam; PF05117; Thermopain; 1.
KV Complete proteome; Hypothetical protein.
CX SEQUENCE 1062 AA; 118024 MW; 166F4ED60A040B4 CRC64;
SO

Query Match 70.0%; Score 42; DB 2; Length 1062;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 70.0%; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TYYFGL 9
DB 623 TYYFGL 629

RESULT 14
O4FWX4_LEIMA PRELIMINARY; PRT; 3212 AA.
AC O4FWX4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=LMJ_1075;
OS Leishmania major.
OC Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
CX NCBI_TaxID=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RX PubMed=16020728; DOI=10.1126/science.1112680;
RA Ivens A.C., Peacock C.S., Worthey E.A., Murphy L., Aggarwal G.,
RA Berriman M., Slek E., Rajandream M.A., Adlem E., Aert R., Anupama A.,
RA Apostolou Z., Attipoe P., Baeson N., Bauser C., Beck A., Beverley S.M.,
RA Bianchetti G., Borzym K., Bothe G., Brusch C.V., Collins M.,
RA Cadag E., Clarioni L., Clayton C., Coulson R.M., Cronin A., Cruz A.K.,
RA Davies R.M., De Gaudenzi J., Dobson D.E., Duesterhoeft A.,
RA Fazelina G., Foster N., Frasch A.C., Fraser A., Fuchs M., Gabel C.,
RA Goble A., Goffeau A., Harris D., Hertz-Fowler C., Hilbert H., Horn D.,
RA Huang Y., Klages S., Knights A., Kube M., Larke N., Livyin L.,
RA Lord A., Louie T., Marra M., Masny D., Matthews K., Michaeli S.,
RA Mortram J.C., Miller-Aner S., Munden H., Nelson S., Norbertczak H.,
RA Oliver K., O'Neil S., Penzance M., Pohl T.M., Price C., Furnelle B.,
RA Quail M.A., Rabinowitch E., Reinhardt R., Rieger M., Rinta J.,
RA Robben J., Robertson L., Ruiz J.C., Rutter S., Saunders D.,
RA Schaefer M., Schein J., Schwartz D.C., Seeger K., Seyler A., Sharp S.,
RA Shin H., Sivam D., Squares R., Squares S., Tosato V., Vogt C.,
RA Voicakeert G., Wambut R., Warren T., Wedler H., Woodward J., Zhou S.,
RA Zimmermann W., Smith D.F., Blackwell J.M., Stuart K.D., Barrell B.,
RA Myler P.J.;
RT "The genome of the Kinetoplastid Parasite, Leishmania major.";
RL Science 309:436-442(2005).
DR EMBL, CP000081; AA214369.1; -, Genomic_DNA.
KV Hypothetical protein.
SO SEQUENCE 3212 AA; 342958 MW; E26EA125060F8A6B CRC64;

Query Match 70.0%; Score 42; DB 2; Length 3212;
Best Local Similarity 70.0%; Pred. No. 3.3e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LATYYFGLD 10
DB 164 LAGYYFGVE 173

RESULT 15
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AC O6A0Z1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Related to mercuric reductase.
GN OrderedLocustNames=DP0504;
OS Desulfotalea psychrophila.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacteriales;
CC Desulfobacteriales; Desulfotalea.
CX NCBI_TaxID=84980;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=LSv54 / DSM 12343;
SO

RX PubMed15305914, DOI:10.1111/j.1462-2920.2004.00665.x;
 RA Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
 RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
 RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
 RA Klank H.-P.,
 RT "The genome of *Desulfotalea psychrophila*, a sulfate-reducing bacterium
 from permanently cold Arctic sediments.";
 RL Environ. Microbiol. 6:887-902(2004).
 DR EMBL; CR522870; CAG35233.1; -; Genomic_DNA.
 DR GO; GO:0005737; C:cytoplasm; IEA.
 DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
 DR GO; GO:0050660; F:FAD binding; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR001327; FAD_pyr_redox.
 DR InterPro; IPR000815; Hg_reductase.
 DR InterPro; IPR006162; Ppatine_S.
 DR InterPro; IPR001100; Pyr_redox.
 DR InterPro; IPR004099; Pyr_redox_dim.
 DR Pfam; PF00070; Pyr_redox; 2.
 DR Pfam; PF02852; Pyr_redox_dim; 1.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00945; HGRDTASE.
 DR PRINTS; PR00411; PNDRDTASEI.
 DR ProDom; PD000139; FAD_pyr_redox; 1.
 DR PROSITE; PS00012; PHOSPHOPANTHETINE; UNKNOWN_1.
 DR PROSITE; PS00076; PYRIDINE_REDOX_1; 1.
 KW Complete proteome.
 SQ SEQUENCE 716 AA; 78725 MW; 68EFC060DBE44094 CRC64;

Query Match 68.3%; Score 41; DB 2; Length 716;
 Best Local Similarity 60.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LATYYFGSD 10
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 DB 14 VSATYFGSD 23

Search completed: December 4, 2005, 04:52:20
 Job time : 104.375 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 03:59:51 : Search time 23.6042 Seconds
(without alignments)
38.528 Million cell updates/sec

Title: US-10-632-706-127
Perfect score: 60
Sequence: 1 LATYYFGGLDV 11

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *
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6: /cgn2_6/ptodata/1/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	71.7	33	1 US-08-053-131-78	Sequence 78, App1
2	43	71.7	33	1 US-08-645-641-78	Sequence 78, App1
3	43	71.7	33	1 US-07-853-408B-78	Sequence 78, App1
4	43	71.7	33	1 US-08-096-762-78	Sequence 78, App1
5	43	71.7	33	1 US-08-308-865-78	Sequence 78, App1
6	43	71.7	33	2 US-09-042-353-275	Sequence 275, App
7	43	71.7	33	2 US-08-758-417A-123	Sequence 123, App
8	43	71.7	33	4 PCT-US92-10983-78	Sequence 78, App1
9	43	71.7	125	2 US-09-840-459-84	Sequence 84, App1
10	43	71.7	125	2 US-09-497-625A-84	Sequence 84, App1
11	42	70.0	29	1 US-08-053-131-73	Sequence 73, App1
12	42	70.0	29	1 US-08-645-641-73	Sequence 73, App1
13	42	70.0	29	1 US-07-853-408B-73	Sequence 73, App1
14	42	70.0	29	1 US-08-096-762-73	Sequence 73, App1
15	42	70.0	29	1 US-08-308-865-73	Sequence 73, App1
16	42	70.0	29	2 US-09-042-353-270	Sequence 270, App
17	42	70.0	29	2 US-08-758-417A-118	Sequence 118, App
18	42	70.0	29	4 PCT-US92-10983-73	Sequence 73, App1
19	42	70.0	31	1 US-08-053-131-83	Sequence 83, App1
20	42	70.0	31	1 US-08-645-641-83	Sequence 83, App1
21	42	70.0	31	1 US-07-853-408B-83	Sequence 83, App1
22	42	70.0	31	1 US-08-758-417A-129	Sequence 84, App1
23	42	70.0	31	1 US-08-096-762-83	Sequence 83, App1
24	42	70.0	31	1 US-08-308-865-83	Sequence 83, App1
25	42	70.0	31	2 US-09-042-353-280	Sequence 280, App
26	42	70.0	31	2 US-08-758-417A-128	Sequence 128, App
27	42	70.0	36	1 PCT-US92-10983-83	Sequence 83, App1
				US-08-053-131-84	Sequence 84, App1

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30	42	70.0	36	1 US-08-096-762-84	Sequence 84, App1
31	42	70.0	36	1 US-08-308-865-84	Sequence 84, App1
32	42	70.0	36	2 US-09-042-353-281	Sequence 281, App
33	42	70.0	36	2 US-08-758-417A-129	Sequence 84, App1
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36	42	70.0	119	2 US-09-497-625A-88	Sequence 88, App1
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38	42	70.0	128	2 US-09-840-459-79	Sequence 79, App1
39	42	70.0	128	2 US-09-497-625A-77	Sequence 77, App1
40	42	70.0	128	2 US-09-497-625A-79	Sequence 79, App1
41	42	70.0	167	2 US-09-472-087-80	Sequence 80, App1
42	42	70.0	236	2 US-09-456-090A-64	Sequence 64, App1
43	42	70.0	236	2 US-09-456-090A-104	Sequence 104, App
44	42	70.0	236	2 US-09-453-234-64	Sequence 64, App1
45	42	70.0	236	2 US-09-453-234-104	Sequence 104, App

ALIGNMENTS

RESULT 1
US-08-053-131-78
: Sequence 78, Application US/08053131
: Patent No. 5661016
: GENERAL INFORMATION:
: APPLICANT: Lomborg, Nila
: APPLICANT: Kay, Robert M.
: TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
: TITLE OF INVENTION: Producing Heterologous Antibodies
: NUMBER OF SEQUENCES: 197
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Kourile and Crew
: STREET: One Market Plaza, Stewart Tower, Suite 200
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94105
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/053,131
: FILING DATE: 26-APR-1993
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/990,860
: FILING DATE: 16-DEC-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/810,279
: FILING DATE: 17-DEC-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/853,408
: FILING DATE: 18-MAR-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M.
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 14643-9-3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-326-2400
: TELEFAX: 415-326-2422
: INFORMATION FOR SEQ ID NO: 78:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 33 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-053-131-78

Query Match 71.7% Score 43; DB 1; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYFGLDV 11
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Db 10 SYYYGMDV 18

RESULT 2

US-08-645-641-78
; Sequence 78, Application US/08645641
; Patent No. 5719032
; GENERAL INFORMATION:
; APPLICANT: Lomborg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,641
; FILING DATE: 20-MAY-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-000913
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2422
; TELEFAX: 415-326-2400
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-645-641-78

Query Match 71.7% Score 43; DB 1; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYFGLDV 11
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Db 10 SYYYGMDV 18

RESULT 3

US-07-853-408B-78
; Sequence 78, Application US/07853408B
; Patent No. 5789650
; GENERAL INFORMATION:
; APPLICANT: Lomborg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies

NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Stewart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/853,408B
; FILING DATE: 19920318
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-853-408B-78

Query Match 71.7% Score 43; DB 1; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYFGLDV 11
:||||:|
Db 10 SYYYGMDV 18

RESULT 4

US-08-096-762-78
; Sequence 78, Application US/08096762
; Patent No. 5814318
; GENERAL INFORMATION:
; APPLICANT: Lomborg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Stewart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,762
; FILING DATE: 22-JUL-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860

;; FILING DATE: 16-DEC-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/904,068
;; FILING DATE: 23-JUN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/853,408
;; FILING DATE: 18-MAR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/810,279
;; FILING DATE: 17-DEC-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M.
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 14643-9-4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-326-2400
;; TELEFAX: 415-326-2422
;; INFORMATION FOR SEQ ID NO: 78:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 33 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-096-762-78

Query Match 71.7%; Score 43; DB 1; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYTFFGLDV 11
:||||:|
Db 10 SYTYGMDV 18

RESULT 5
US-08-308-865-78
; Sequence 78, Application US/08308865
; Patent No. 5877397
; GENERAL INFORMATION:
; APPLICANT: Lomborg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent'n Release #1.0, Version #1.25
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; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,707
; FILING DATE:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422

;; INFORMATION FOR SEQ ID NO: 78:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 33 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-308-865-78

Query Match 71.7%; Score 43; DB 1; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYTFFGLDV 11
:||||:|
Db 10 SYTYGMDV 18

RESULT 6
US-09-042-353-275
; Sequence 275, Application US/09042353
; Patent No. 6255458
; GENERAL INFORMATION:
; APPLICANT: Lomborg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 421
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent'n Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,353
; FILING DATE: 13-MAR-1998
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/810,279
; FILING DATE: 17-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,408
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/209,741

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      FILING DATE: 09-MAR-1994
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/352,322
      FILING DATE: 07-DEC-1994
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/544,404
      FILING DATE: 10-OCT-1995
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/728,463
      FILING DATE: 10-OCT-1996
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: WO PCT/US96/16433
      FILING DATE: 10-OCT-1996
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/758,417
      FILING DATE: 02-DEC-1996
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: WO PCT/US97/21803
      FILING DATE: 01-DEC-1997
      ATTORNEY/AGENT INFORMATION:
      NAME: Apple, Randolph T.
      REGISTRATION NUMBER: 36,429
      REFERENCE/DOCKET NUMBER: 014643-009040US
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (415) 576-0200
      TELEFAX: (415) 576-0300
      INFORMATION FOR SEQ ID NO: 275:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 33 amino acids
      TYPE: amino acid
      STRANDEDNESS:
      TOPOLOGY: linear
      MOLECULE TYPE: peptide
      US-09-042-353-275

Query Match      71.7%; Score 43; DB 2; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      3 TTYVFGLDV 11
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Db      10 SYYYGMDV 18

RESULT 7
US-08-758-417A-123
; Sequence 123, Application US/08758417A
; Patent No. 6300129
; GENERAL INFORMATION:
; APPLICANT: Lomborg, Nils
; Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
; Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 417
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-5834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,417A
; FILING DATE: 02-DEC-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/728,463
; FILING DATE: 10-OCT-1996
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      APPLICATION NUMBER: US 08/544,404
      FILING DATE: 10-OCT-1995
      APPLICATION NUMBER: US 08/352,322
      FILING DATE: 07-DEC-1994
      APPLICATION NUMBER: US 08/209,741
      FILING DATE: 09-MAR-1994
      APPLICATION NUMBER: US 08/165,699
      FILING DATE: 10-DEC-1993
      APPLICATION NUMBER: US 08/161,739
      FILING DATE: 03-DEC-1993
      APPLICATION NUMBER: US 08/155,301
      FILING DATE: 18-NOV-1993
      APPLICATION NUMBER: US 08/096,762
      FILING DATE: 22-JUL-1993
      APPLICATION NUMBER: US 08/053,131
      FILING DATE: 26-APR-1993
      APPLICATION NUMBER: US 07/990,860
      FILING DATE: 16-DEC-1992
      ATTORNEY/AGENT INFORMATION:
      NAME: Serafini, Andrew T.
      REGISTRATION NUMBER: 41,303
      REFERENCE/DOCKET NUMBER: 014643-009030US
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (415) 576-0200
      TELEFAX: (415) 576-0300
      INFORMATION FOR SEQ ID NO: 123:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 33 amino acids
      TYPE: amino acid
      STRANDEDNESS: <Unknown>
      TOPOLOGY: linear
      MOLECULE TYPE: peptide
      SEQUENCE DESCRIPTION: SEQ ID NO: 123:
      US-08-758-417A-123

Query Match      71.7%; Score 43; DB 2; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      3 TTYVFGLDV 11
      :|||:|||
Db      10 SYYYGMDV 18

RESULT 8
PCT-US92-10983-78
; Sequence 78, Application PC/TV9210983
; GENERAL INFORMATION:
; APPLICANT: Lomborg, Nils
; Kay, Robert M.
; TITLE OF INVENTION: Transgenic Non-Human Animals for
; Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 152
; CORRESPONDENCE ADDRESS:
; ADDRESSER: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10983
; FILING DATE: 19921217
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9-2
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US92-10983-78

Query Match 71.7%; Score 43; DB 4; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYTGGADV 11
Db 10 SYTYGMDV 18

RESULT 9
US-09-840-459-84
Sequence 84, Application US/09840459
Patent No. 6696550
GENERAL INFORMATION:
APPLICANT: Larosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 84
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
US-09-840-459-84

Query Match 71.7%; Score 43; DB 2; Length 125;
Best Local Similarity 66.7%; Pred. No. 6.4;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYTGGADV 11
Db 106 SYTYGMDV 114

RESULT 10
US-09-497-625A-84
Sequence 84, Application US/09497625A
Patent No. 6727349
GENERAL INFORMATION:
APPLICANT: Larosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa

TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-004
CURRENT APPLICATION NUMBER: US/09/497,625A
CURRENT FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 84
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
US-09-497-625A-84

Query Match 71.7%; Score 43; DB 2; Length 125;
Best Local Similarity 66.7%; Pred. No. 6.4;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYTGGADV 11
Db 106 SYTYGMDV 114

RESULT 11
US-08-053-131-73
Sequence 73, Application US/08053131
Patent No. 5661016
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 200
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,131
FILING DATE: 26-APR-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-053-131-73

Query Match 70.0%; Score 42; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 2.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
|||:|:|
DB 7 YYYGMDV 14

RESULT 12
US-08-645-641-73
Sequence 73, Application US/08645641
Patent No. 5719032
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSER: William M. Smith
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,641
FILING DATE: 20-MAY-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-000913
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-645-641-73

Query Match 70.0%; Score 42; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 2.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
|||:|:|
DB 7 YYYGMDV 14

RESULT 13
US-07-853-408B-73
Sequence 73, Application US/07853408B
Patent No. 5789650
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils

APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSER: William M. Smith
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/853,408B
FILING DATE: 19920318
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2422
TELEFAX: 415-326-2400
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-853-408B-73

Query Match 70.0%; Score 42; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 2.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
|||:|:|
DB 7 YYYGMDV 14

RESULT 14
US-08-096-762-73
Sequence 73, Application US/08096762
Patent No. 5814318
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend Kourile and Crew
STREET: One Market Plaza, Stewart Tower, Suite 200
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,762
FILING DATE: 22-JUL-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131

FILED DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-096-762-73

Query Match 70.0%; Score 42; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 2.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYFGLDV 11
|||:|:
Db 7 YYYGMDV 14

RESULT 15
US-08-308-865-73
Sequence 73, Application US/08308865
Patent No. 5877397
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESSES:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,865
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/145,707
FILING DATE:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-1-1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-308-865-73

Query Match 70.0%; Score 42; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 2.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYFGLDV 11
|||:|:
Db 7 YYYGMDV 14

Search completed: December 4, 2005, 04:09:43
Job time : 24.6042 secs

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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:07:28 ; Search time 78.833 Seconds
(without alignments)
58.302 Million cell updates/sec

Title: US-10-632-706-127
Perfect score: 60
Sequence: 1 LATYVFGLDV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	11	4	US-10-632-706-126
2	60	100.0	11	4	US-10-632-706-127
3	48	80.0	122	6	US-11-031-485-116
4	47	78.3	129	4	US-10-364-743-101
5	47	78.3	129	5	US-10-452-593-101
6	47	78.3	134	4	US-10-364-743-15
7	47	78.3	134	5	US-10-452-593-15
8	47	78.3	468	6	US-11-031-485-56
9	47	78.3	469	6	US-11-031-485-18
10	46	76.7	13	4	US-10-632-706-114
11	46	76.7	21	5	US-10-783-311-141
12	46	76.7	140	5	US-10-783-311-115
13	45	75.0	16	5	US-10-783-311-277
14	45	75.0	21	3	US-09-880-748-3068
15	45	75.0	21	4	US-10-293-418-3068
16	45	75.0	117	6	US-11-009-731-47
17	45	75.0	135	5	US-10-783-311-271
18	45	75.0	256	5	US-09-880-748-1600
19	45	75.0	256	4	US-10-293-418-1600
20	44	73.3	16	3	US-09-880-748-2129
21	44	73.3	16	4	US-10-293-418-2129
22	44	73.3	17	3	US-09-880-748-2876
23	44	73.3	17	4	US-10-293-418-2876
24	44	73.3	18	5	US-10-984-960A-8
25	44	73.3	117	4	US-10-041-860-206
26	44	73.3	123	4	US-10-309-762-18
27	44	73.3	123	4	US-10-309-762-19

28	44	73.3	124	4	US-10-292-088-106	Sequence 106, App
29	44	73.3	127	4	US-10-041-860-31	Sequence 31, App1
30	44	73.3	127	4	US-10-041-860-243	Sequence 243, App
31	44	73.3	127	4	US-10-041-860-325	Sequence 325, App
32	44	73.3	127	4	US-10-665-383-42	Sequence 42, App1
33	44	73.3	127	4	US-10-466-242-53	Sequence 53, App1
34	44	73.3	127	5	US-10-984-960A-2	Sequence 2, App11
35	44	73.3	129	4	US-10-292-088-10	Sequence 10, App1
36	44	73.3	134	4	US-10-364-743-16	Sequence 16, App1
37	44	73.3	134	4	US-10-364-743-109	Sequence 109, App
38	44	73.3	134	4	US-10-364-743-110	Sequence 110, App
39	44	73.3	134	5	US-10-452-593-16	Sequence 16, App1
40	44	73.3	134	5	US-10-452-593-109	Sequence 109, App
41	44	73.3	134	5	US-10-452-593-110	Sequence 110, App
42	44	73.3	145	5	US-10-644-277-146	Sequence 146, App
43	44	73.3	157	5	US-10-473-287-34	Sequence 34, App1
44	44	73.3	157	5	US-10-473-287-63	Sequence 63, App1
45	44	73.3	249	5	US-10-935-290-61	Sequence 61, App1

ALIGNMENTS

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RESULT 1
US-10-632-706-126
; Sequence 126, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 126
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-126
Query Match 100.0%; Score 60; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 LATYVFGLDV 11
Db 1 LATYVFGLDV 11
RESULT 2
US-10-632-706-127
; Sequence 127, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
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;; PRIOR FILING DATE: 1998-08-31
;; NUMBER OF SEQ ID NOS: 278
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO: 127
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-127

Query Match 100.0%; Score 60; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LATYYFGLDV 11
|||
Db 1 LATYYFGLDV 11

RESULT 3
US-11-031-485-116
; Sequence 116, Application US/11031485
; Publication No. US20050232917A1
; GENERAL INFORMATION:
; APPLICANT: PULLEN, NICHOLAS
; APPLICANT: MOLLOY, ELIZABETH
; APPLICANT: KEILERMANN, SIRID-AIMEE
; APPLICANT: GREEN, LARRY L.
; APPLICANT: HAAK-FRENSCH, MARY
; TITLE OF INVENTION: ANTIBODIES TO MADCAM
; FILE REFERENCE: ABX-PF6
; CURRENT APPLICATION NUMBER: US/11/031,485
; PRIOR FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: 60/535,490
; PRIOR FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO: 116
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-031-485-116

Query Match 80.0%; Score 48; DB 6; Length 122;
Best Local Similarity 63.6%; Pred. No. 2.8;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LATYYFGLDV 11
: |||: |||
Db 100 VVYYYYGMDV 110

RESULT 4
US-10-364-743-101
; Sequence 101, Application US/10364743
; Publication No. US20040009178A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: NO. US20040009178A1an, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 84 (1087-73)
; CURRENT APPLICATION NUMBER: US/10/364,743
; PRIOR FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 101
; LENGTH: 129

;; TYPE: PRT
;; ORGANISM: human
US-10-364-743-101

Query Match 78.3%; Score 47; DB 4; Length 129;
Best Local Similarity 77.8%; Pred. No. 4.4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TYYVFGLDV 11
|||: |||
Db 105 TYYVYGMDV 113

RESULT 5
US-10-452-593-101
; Sequence 101, Application US/10452593
; Publication No. US20040258699A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: Nolan, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 98 CIP (1087-73 CIP)
; CURRENT APPLICATION NUMBER: US/10/452,593
; PRIOR FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 10/364,743
; PRIOR FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/356,086
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/376,408
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 101
; LENGTH: 129
; TYPE: PRT
; ORGANISM: human
US-10-452-593-101

Query Match 78.3%; Score 47; DB 5; Length 129;
Best Local Similarity 77.8%; Pred. No. 4.4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TYYVFGLDV 11
|||: |||
Db 105 TYYVYGMDV 113

RESULT 6
US-10-364-743-15
; Sequence 15, Application US/10364743
; Publication No. US20040009178A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: NO. US20040009178A1an, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 84 (1087-73)
; CURRENT APPLICATION NUMBER: US/10/364,743
; PRIOR FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 15
; LENGTH: 134
; TYPE: PRT

ORGANISM: human
US-10-364-743-15

Query Match 78.3%; Score 47; DB 4; Length 134;
Best Local Similarity 77.8%; Pred. No. 4.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTGGLDV 11
|||:|:
DB 110 TTYTGGMDV 118

RESULT 7

US-10-452-593-15
Sequence 15, Application US/10452593
Publication No. US20040258699A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Wild, Martha A.
APPLICANT: Maruyama, Toshiaki
APPLICANT: Nolan, Mary Jean
TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
FILE REFERENCE: 98 CIP (1087-73 CIP)
CURRENT APPLICATION NUMBER: US/10/452,593
CURRENT FILING DATE: 2003-06-02
PRIOR APPLICATION NUMBER: US 10/364,743
PRIOR FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US 60/356,086
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/376,408
PRIOR FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: US 60/428,807
PRIOR FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.2
SEQ ID NO 15
LENGTH: 134
TYPE: PRT
ORGANISM: human
US-10-452-593-15

Query Match 78.3%; Score 47; DB 5; Length 134;
Best Local Similarity 77.8%; Pred. No. 4.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTGGLDV 11
|||:|:
DB 110 TTYTGGMDV 118

RESULT 8

US-11-031-485-56
Sequence 56, Application US/11031485
Publication No. US20050232917A1
GENERAL INFORMATION:
APPLICANT: PULLEN, NICHOLAS
APPLICANT: MOLLOY, ELIZABETH
APPLICANT: KELLERMANN, SIRID-AIMEE
APPLICANT: GREEN, LARRY L.
APPLICANT: HAAK-FREDSCHO, MARY
TITLE OF INVENTION: ANTIBODIES TO MADCAM
FILE REFERENCE: ABX-PF6
CURRENT APPLICATION NUMBER: US/11/031,485
CURRENT FILING DATE: 2005-01-07
PRIOR APPLICATION NUMBER: 60/535,490
PRIOR FILING DATE: 2004-01-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 56
LENGTH: 468
TYPE: PRT
ORGANISM: Homo sapiens

US-11-031-485-56

Query Match 78.3%; Score 47; DB 6; Length 468;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTGGLDV 11
|||:|:
DB 123 TTYTGGMDV 131

RESULT 9

US-11-031-485-18
Sequence 18, Application US/11031485
Publication No. US20050232917A1
GENERAL INFORMATION:
APPLICANT: PULLEN, NICHOLAS
APPLICANT: MOLLOY, ELIZABETH
APPLICANT: KELLERMANN, SIRID-AIMEE
APPLICANT: GREEN, LARRY L.
APPLICANT: HAAK-FREDSCHO, MARY
TITLE OF INVENTION: ANTIBODIES TO MADCAM
FILE REFERENCE: ABX-PF6
CURRENT APPLICATION NUMBER: US/11/031,485
CURRENT FILING DATE: 2005-01-07
PRIOR APPLICATION NUMBER: 60/535,490
PRIOR FILING DATE: 2004-01-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 18
LENGTH: 469
TYPE: PRT
ORGANISM: Homo sapiens
US-11-031-485-18

Query Match 78.3%; Score 47; DB 6; Length 469;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTGGLDV 11
|||:|:
DB 123 TTYTGGMDV 131

RESULT 10

US-10-632-706-114
Sequence 114, Application US/10632706
Publication No. US20040175385A1
GENERAL INFORMATION:
APPLICANT: MARKS, JAMES D.
APPLICANT: AMERSDORFER, PETER
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
FILE REFERENCE: 407T-895120US
CURRENT APPLICATION NUMBER: US/10/632,706
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US 60/400,721
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 09/144,806
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 114
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial
FEATURES:
OTHER INFORMATION: single chain antibody fragment
US-10-632-706-114

Query Match 76.7%; Score 46; DB 4; Length 13;
Best Local Similarity 70.0%; Pred. No. 0.64;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db      4 ANYYYGMDV 13

RESULT 11
US-10-783-311-141
; Sequence 141, Application US/10783311
; Publication No. US2005009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 141
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy Chain amino acid sequence
US-10-783-311-141

Query Match      76.7%; Score 46; DB 5; Length 21;
Best Local Similarity 63.6%; Pred. No. 1;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 LATYYFGLDV 11
      |||:|:|
Db      11 LGNYYYGMDV 21

RESULT 12
US-10-783-311-135
; Sequence 135, Application US/10783311
; Publication No. US2005009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy Chain amino acid sequence
US-10-783-311-135

Query Match      76.7%; Score 46; DB 5; Length 140;
Best Local Similarity 63.6%; Pred. No. 6.9;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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; Publication No. US2005009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 277
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy Chain amino acid sequence
US-10-783-311-277

Query Match      75.0%; Score 45; DB 5; Length 16;
Best Local Similarity 63.6%; Pred. No. 1.2;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 LATYYFGLDV 11
      |||:|:|
Db      6 VAGYYYGMDV 16

RESULT 14
US-09-880-748-3068
; Sequence 3068, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3068
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-3068

Query Match      75.0%; Score 45; DB 3; Length 21;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 ATYYFGLDV 11
      |||:|:|
Db      12 APYYYGMDV 21

RESULT 15
US-10-293-418-3068
; Sequence 3068, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
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; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3068
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-3068

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Query Match      75.0%; Score 45; DB 4; Length 21;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY      2 ATYYFGADV 11
        | |||: |||
Db      12 APYYGMDV 21

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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:08:08 ; Search time 3.20833 Seconds
(without alignments)
16.417 Million cell updates/sec

Title: US-10-632-706-127

Perfect score: 60
Sequence: 1 LATYYFGGLDV 11

Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	45	75.0	21 7 US-11-054-515-3068	Sequence 3068, Ap
2	45	75.0	256 7 US-11-054-515-1600	Sequence 1600, Ap
3	44	73.3	16 7 US-11-054-515-2129	Sequence 2129, Ap
4	44	73.3	17 7 US-11-054-515-2876	Sequence 2876, Ap
5	44	73.3	252 7 US-11-054-515-1431	Sequence 1431, Ap
6	44	73.3	254 7 US-11-054-515-3	Sequence 3, Appl1
7	44	73.3	254 7 US-11-054-515-838	Sequence 838, App
8	44	73.3	254 7 US-11-054-515-870	Sequence 870, App
9	44	73.3	254 7 US-11-054-515-1287	Sequence 1287, App
10	44	73.3	254 7 US-11-054-515-1288	Sequence 1288, App
11	43	71.7	306 7 US-11-017-550-47	Sequence 47, Appl
12	42	70.0	13 7 US-11-054-515-3091	Sequence 3091, Ap
13	42	70.0	17 7 US-11-054-515-2817	Sequence 2817, Ap
14	42	70.0	19 7 US-11-054-515-2735	Sequence 2735, Ap
15	42	70.0	19 7 US-11-054-515-2899	Sequence 2899, Ap
16	42	70.0	19 7 US-11-054-515-2928	Sequence 2928, Ap
17	42	70.0	19 7 US-11-054-515-2935	Sequence 2935, Ap
18	42	70.0	19 7 US-11-054-515-3038	Sequence 3038, Ap
19	42	70.0	19 7 US-11-054-515-3052	Sequence 3052, Ap
20	42	70.0	19 7 US-11-054-515-3067	Sequence 3067, Ap
21	42	70.0	19 7 US-11-054-515-3087	Sequence 3087, Ap
22	42	70.0	19 7 US-11-054-515-3145	Sequence 3145, Ap
23	42	70.0	20 7 US-11-040-159-4	Sequence 4, Appl1
24	42	70.0	20 7 US-11-054-515-2767	Sequence 2767, Ap
25	42	70.0	20 7 US-11-054-515-3039	Sequence 3039, Ap

26	42	70.0	24 7 US-11-054-515-2926	Sequence 2926, Ap
27	42	70.0	124 7 US-11-144-248-8	Sequence 8, Appl1
28	42	70.0	125 7 US-11-144-248-16	Sequence 16, Appl1
29	42	70.0	174 7 US-11-144-248-4	Sequence 4, Appl1
30	42	70.0	248 7 US-11-054-515-1965	Sequence 1965, Ap
31	42	70.0	248 7 US-11-054-515-1974	Sequence 1974, Ap
32	42	70.0	251 7 US-11-054-515-1315	Sequence 1315, Ap
33	42	70.0	251 7 US-11-054-515-1740	Sequence 1740, Ap
34	42	70.0	251 7 US-11-054-515-1921	Sequence 1921, Ap
35	42	70.0	252 7 US-11-054-515-1731	Sequence 1731, Ap
36	42	70.0	253 7 US-11-054-515-934	Sequence 934, App
37	42	70.0	254 7 US-11-054-515-1001	Sequence 1001, Ap
38	42	70.0	254 7 US-11-054-515-1259	Sequence 1259, Ap
39	42	70.0	254 7 US-11-054-515-1334	Sequence 1334, Ap
40	42	70.0	254 7 US-11-054-515-1701	Sequence 1701, Ap
41	42	70.0	254 7 US-11-054-515-1735	Sequence 1735, Ap
42	42	70.0	254 7 US-11-054-515-1739	Sequence 1739, Ap
43	42	70.0	255 7 US-11-054-515-1271	Sequence 1271, Ap
44	42	70.0	255 7 US-11-054-515-1284	Sequence 1284, Ap
45	42	70.0	256 7 US-11-054-515-1209	Sequence 1209, Ap

ALIGNMENTS

RESULT 1
US-11-054-515-3068
Sequence 3068, Application US/11054515
Publication No. US2005025532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: p5523p3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 3068
LENGTH: 21
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-3068
Query Match 75.0%; Score 45; DB 7; Length 21;
Best Local Similarity 70.0%; Pred. No. 0.017;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Oy 2 ATYYFGGLDV 11
Db 12 APYYIGMDV 21
RESULT 2

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US-11-054-515-1600
; Sequence 1600, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1600
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1600

Query Match          75.0%; Score 45; DB 7; Length 256;
Best Local Similarity 70.0%; Pred. No. 0.19;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      2 ATYYFGLDV 11
|  |||:|:|
Db      110 APYYTGMDV 119

RESULT 3
US-11-054-515-2129
; Sequence 2129, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2876
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2876

Query Match          73.3%; Score 44; DB 7; Length 17;
Best Local Similarity 63.6%; Pred. No. 0.021;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2129
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2129

Query Match          73.3%; Score 44; DB 7; Length 16;
Best Local Similarity 63.6%; Pred. No. 0.02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 LATYYFGLDV 11
|  |||:|:|
Db      6 LTGYTYGMDV 16

RESULT 4
US-11-054-515-2876
; Sequence 2876, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2876
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2876

Query Match          73.3%; Score 44; DB 7; Length 17;
Best Local Similarity 63.6%; Pred. No. 0.021;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 LATYYFGLDV 11
|  |||:|:|
Db      7 LTGYTYGMDV 17

RESULT 5
US-11-054-515-1431
; Sequence 1431, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
```

```
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523P3
;; CURRENT APPLICATION NUMBER: US/11/054,515
;; CURRENT FILING DATE: 2005-02-10
;; PRIOR APPLICATION NUMBER: 60/543,296
;; PRIOR FILING DATE: 2004-02-11
;; PRIOR APPLICATION NUMBER: 60/580,347
;; PRIOR FILING DATE: 2004-06-18
;; PRIOR APPLICATION NUMBER: 10/293,418
;; PRIOR FILING DATE: 2002-11-14
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 1431
;; LENGTH: 252
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-054-515-1431
```

```
Query Match      73.3% Score 44; DB 7; Length 252;
Best Local Similarity 63.6%; Pred. No. 0.28;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 LATYYFGLDV 11
Db      105 LTGYYYGMDV 115
```

```
RESULT 6
US-11-054-515-3
;; Sequence 3, Application US/11054515
;; Publication No. US20050255532A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523P3
;; CURRENT APPLICATION NUMBER: US/11/054,515
;; CURRENT FILING DATE: 2005-02-10
;; PRIOR APPLICATION NUMBER: 60/543,296
;; PRIOR FILING DATE: 2004-02-11
;; PRIOR APPLICATION NUMBER: 60/580,347
;; PRIOR FILING DATE: 2004-06-18
;; PRIOR APPLICATION NUMBER: 10/293,418
;; PRIOR FILING DATE: 2002-11-14
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 3247
```

```
;; SEQ ID NO 3
;; LENGTH: 254
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-054-515-3
```

```
Query Match      73.3% Score 44; DB 7; Length 254;
Best Local Similarity 63.6%; Pred. No. 0.28;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 LATYYFGLDV 11
Db      107 LTGYYYGMDV 117
```

```
RESULT 7
US-11-054-515-838
;; Sequence 838, Application US/11054515
;; Publication No. US20050255532A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523P3
;; CURRENT APPLICATION NUMBER: US/11/054,515
;; CURRENT FILING DATE: 2005-02-10
;; PRIOR APPLICATION NUMBER: 60/543,296
;; PRIOR FILING DATE: 2004-02-11
;; PRIOR APPLICATION NUMBER: 60/580,347
;; PRIOR FILING DATE: 2004-06-18
;; PRIOR APPLICATION NUMBER: 10/293,418
;; PRIOR FILING DATE: 2002-11-14
;; PRIOR APPLICATION NUMBER: 60/331,469
;; PRIOR FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/340,817
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 09/880,748
;; PRIOR FILING DATE: 2001-06-15
;; PRIOR APPLICATION NUMBER: 60/293,499
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/277,379
;; PRIOR FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: 60/276,248
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/240,816
;; PRIOR FILING DATE: 2000-10-17
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 3247
;; SEQ ID NO 838
;; LENGTH: 254
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-054-515-838
```

```
Query Match      73.3% Score 44; DB 7; Length 254;
Best Local Similarity 63.6%; Pred. No. 0.28;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      1 LATYYFGLDV 11
Db      107 LTGYYYGMDV 117
```

```
RESULT 8
US-11-054-515-870
;; Sequence 870, Application US/11054515
;; Publication No. US20050255532A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
;; FILE REFERENCE: PF523P3
;; CURRENT APPLICATION NUMBER: US/11/054,515
;; CURRENT FILING DATE: 2005-02-10
;; PRIOR APPLICATION NUMBER: 60/543,296
```

```
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 870
/ LENGTH: 254
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: Site
/ LOCATION: (42)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ FEATURE:
/ NAME/KEY: Site
/ LOCATION: (45)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ FEATURE:
/ NAME/KEY: Site
/ LOCATION: (51)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ FEATURE:
/ NAME/KEY: Site
/ LOCATION: (57)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ FEATURE:
/ NAME/KEY: Site
/ LOCATION: (65)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ FEATURE:
/ NAME/KEY: Site
/ LOCATION: (67)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ FEATURE:
/ NAME/KEY: Site
/ LOCATION: (70)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ FEATURE:
/ NAME/KEY: Site
/ LOCATION: (170)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ FEATURE:
/ NAME/KEY: Site
/ LOCATION: (176)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ FEATURE:
/ NAME/KEY: Site
/ LOCATION: (192)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ FEATURE:
/ NAME/KEY: Site
/ LOCATION: (235)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ FEATURE:
/ NAME/KEY: Site
/ LOCATION: (239)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
```

```
/ FEATURE:
/ NAME/KEY: Site
/ LOCATION: (240)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-11-054-515-870

Query Match 73.3% Score 44; DB 7; Length 254;
Best Local Similarity 63.6% Pred. No. 0.28;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Cy 1 LATYYFGADV 11
Db 107 LTGYTYGMDV 117

RESULT 9
US-11-054-515-1287
Sequence 1287, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P3
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1287
LENGTH: 254
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1287

Query Match 73.3% Score 44; DB 7; Length 254;
Best Local Similarity 63.6% Pred. No. 0.28;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Cy 1 LATYYFGADV 11
Db 107 LTGYTYGMDV 117

RESULT 10
US-11-054-515-1288
Sequence 1288, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P3
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
```

PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1288
LENGTH: 254
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1288

Query Match 73.3%; Score 44; DB 7; Length 254;
Best Local Similarity 63.6%; Pred. No. 0.28;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 LATYYFGLDV 11
Db 107 LTYTYGMDV 117

RESULT 11
US-11-017-550-47
Sequence 47, Application US/11017550
Publication No. US20050250183A1
GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
APPLICANT: Schultz, Peter G
APPLICANT: Wang, Lei
APPLICANT: Anderson, John C
APPLICANT: Chin, Jason
APPLICANT: Liu, David R
APPLICANT: Magliery, Thomas
APPLICANT: Meggers, Eric L
APPLICANT: Mehl, Ryan A
APPLICANT: Paetznak, Miro
APPLICANT: Santoro, Stephen W
TITLE OF INVENTION: In Vivo Incorporation of Unnatural Amino Acids
FILE REFERENCE: 54-000120US
CURRENT APPLICATION NUMBER: US/11/017,550
CURRENT FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: US/10/126,927
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/285,030
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 60/355,514
PRIOR FILING DATE: 2002-02-06
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn version 3.1
SEQ ID NO 47
LENGTH: 306
TYPE: PRT
ORGANISM: Methanococcus jannaschii
US-11-017-550-47

Query Match 71.7%; Score 43; DB 7; Length 306;
Best Local Similarity 77.8%; Pred. No. 0.5;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy 3 TYYYFGLDV 11
Db 158 TTYTLGVGV 166

RESULT 12
US-11-054-515-3091
Sequence 3091, Application US/11054515
Publication No. US2005025532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: P5523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
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PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 3091
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-3091

Query Match 70.0%; Score 42; DB 7; Length 13;
Best Local Similarity 75.0%; Pred. No. 0.035;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 4 YYYFGLDV 11
Db 6 YYYGMDV 13

RESULT 13
US-11-054-515-2817
Sequence 2817, Application US/11054515
Publication No. US2005025532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: P5523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817

```
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO: 2817
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2817
```

```
Query Match      70.0%; Score 42; DB 7; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.046;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 YYYFGLDV 11
      |||:|:|
Db      10 YYYGMDV 17
```

```
RESULT 14
US-11-054-515-2735
/ Sequence 2735; Application US/11054515
/ Publication No. US20050255532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO: 2735
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2735
```

```
Query Match      70.0%; Score 42; DB 7; Length 19;
Best Local Similarity 75.0%; Pred. No. 0.051;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 YYYFGLDV 11
      |||:|:|
Db      12 YYYGMDV 19
```

```
RESULT 15
US-11-054-515-2899
/ Sequence 2899; Application US/11054515
/ Publication No. US20050255532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO: 2899
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2899
```

```
Query Match      70.0%; Score 42; DB 7; Length 19;
Best Local Similarity 75.0%; Pred. No. 0.051;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 YYYFGLDV 11
      |||:|:|
Db      12 YYYGMDV 19
```

```
Search completed: December 4, 2005, 04:37:48
Job time : 3.20833 secs
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:09:54 ; Search time 95.5625 Seconds
(without alignments)
50.576 Million cell updates/sec

Title: US-10-632-706-128

Perfect score: 66

Sequence: 1 GPMELVGYFDS 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

- 1: A_Geneseq_21:*
- 2: geneseqp1980s:*
- 3: geneseqp1990s:*
- 4: geneseqp2000s:*
- 5: geneseqp2001s:*
- 6: geneseqp2002s:*
- 7: geneseqp2003as:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	11	8	ADR38726 Mouse, hea
2	44	66.7	306	6	ABU45531 Protein e
3	44	66.7	367	6	ABU47042 Protein e
4	44	66.7	367	6	ABU47877 Protein e
5	43	65.2	207	8	ADH12894 Francisel
6	42	63.6	415	7	ABM89126 Rice abio
7	41	62.1	114	4	AAO08773 Human pol
8	41	62.1	121	2	AAK88504 Vhm for
9	41	62.1	475	6	ABU20453 Protein e
10	41	62.1	792	7	ADC07986 Rice prot
11	41	62.1	1352	4	ABB67542 Drosophil
12	40	60.6	146	6	ABP56656 Chimpanze
13	40	60.6	283	6	ABM70292 Phototrab
14	40	60.6	477	8	ADY22314 Plant ful
15	40	60.6	885	3	AAK32050 Arabidops
16	40	60.6	931	3	AAK32049 Arabidops
17	40	60.6	956	3	AAK32048 Arabidops
18	39.5	59.8	511	8	ADH89844 Plant ful
19	39	59.1	79	3	AAK13553 Arabidops
20	39	59.1	103	3	AAK13552 Arabidops
21	39	59.1	112	3	AAK13551 Arabidops
22	39	59.1	166	4	AAK06860 Human foe
23	39	59.1	211	8	ADM57065 A thalian
24	39	59.1	233	3	AAK05440 Arabidops

ALIGNMENTS

25	39	59.1	233	3	AAK38801	AAK38801 Arabidops
26	39	59.1	242	5	ABG69053	ABG69053 Amino aci
27	39	59.1	254	3	AAK30761	AAK30761 Arabidops
28	39	59.1	257	3	AAK38800	AAK38800 Arabidops
29	39	59.1	257	3	AAK05439	AAK05439 Arabidops
30	39	59.1	266	3	AAK05438	AAK05438 Arabidops
31	39	59.1	266	3	AAK38799	AAK38799 Arabidops
32	39	59.1	266	5	ABK92172	ABK92172 Herbicida
33	39	59.1	274	9	ABM85054	ABM85054 M. xanthu
34	39	59.1	278	3	AAK30760	AAK30760 Arabidops
35	39	59.1	287	3	AAK30759	AAK30759 Arabidops
36	39	59.1	537	8	ADT60469	ADT60469 Plant pol
37	39	59.1	670	6	ABU18890	ABU18890 Protein e
38	39	59.1	696	4	ABG20404	ABG20404 Novel hum
39	39	59.1	775	4	AAU48754	AAU48754 Propionib
40	39	59.1	775	6	ABM65954	ABM65954 Propionib
41	39	59.1	775	6	ABM45273	ABM45273 Propionib
42	39	59.1	877	3	AAK36913	AAK36913 Arabidops
43	39	59.1	885	3	AAK36912	AAK36912 Arabidops
44	39	59.1	949	3	AAK36911	AAK36911 Arabidops
45	38	57.6	48	4	AAK95055	AAK95055 Human rep

RESULT 1
ADR38726 standard; peptide; 11 AA.
ID ADR38726 standard; peptide; 11 AA.
AC ADR38726;
XX 02-DEC-2004 (first entry)
DE Mouse heavy chain variable region CDR3 seqid 128.
XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;
KW heavy chain variable region; complementarily determining region; CDR3.
XX Mus sp.
OS US2004175385-A1.
PN 09-SEP-2004.
XX 01-AUG-2003; 2003US-00632706.
XX 31-AUG-1998; 98US-00144886.
PR 01-AUG-2002; 2002US-0400721P.
XX (REGC) UNIV CALIFORNIA.
XX Marks JD, Amersdorfer P;
XX WPI; 2004-652009/63.
XX New isolated antibody that neutralizes botulinum neurotoxin type A,
PT useful for diagnosing botulism or for treating pathologies associated
PT with botulinum neurotoxin poisoning.
XX Example 3; SEQ ID NO 128; 110pp; English.
XX The invention describes an isolated antibody (I) that specifically binds
XX to an epitope specifically bound by an antibody expressed by a specific
XX clone where (I) binds to and neutralises botulinum neurotoxin type A
XX (BONT/A). An isolated antibody (I) that specifically binds to an epitope
XX specifically bound by an antibody expressed by a clone chosen from clone
XX S25, C25, C35, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
XX 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
XX neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
XX comprising BONT/A neutralising epitope having an epitope that is

CC specifically bound by an antibody expressed by clones as mentioned in (1)
CC ; producing (1) ; and a composition (11) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplu. The following are disclosed: a pharmaceutical composition
CC comprising (1) ; and a kit comprising (1) . (1) is useful for neutralising
CC Bont/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (1) in surplu, where each of (1) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplu. (1) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (1) exhibits specificity and affinity towards Bont/A. (1)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain variable region complementarity determining
CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 66; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GPMELVGFDS 11
Db 1 GPMELVGFDS 11
RESULT 2
ABU45531
ID ABU45531 standard; protein; 306 AA.
XX
AC ABU45531;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #31058.
XX
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Salmomella paratyphi.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002MO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zvekind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI: 2003-029926/02.
XX
DR N-PSDB; ACA49401.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 73455; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound an antibiotic; (10) profiling a
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 306 AA;
Query Match 66.7%; Score 44; DB 6; Length 306;
Best Local Similarity 69.2%; Pred. No. 40;
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
OY 1 GPMELV----GYF 9
Db 66 GPMELVAGPFGYF 78
RESULT 3
ABU47042
ID ABU47042 standard; protein; 367 AA.
XX
AC ABU47042;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #32569.
XX
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Salmomella typhimurium.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002MO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zvekind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI: 2003-029926/02.
XX
DR N-PSDB; ACA50912.
XX

PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 74966; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 367 AA:
Query Match 66.7%; Score 44; DB 6; Length 367;
Best Local Similarity 69.2%; Pred. No. 48;
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
Qy 1 GPMELV---GYF 9
Db 127 GPMELVLPFGYF 139
RESULT 4
ABU47877
ID ABU47877 standard; protein; 367 AA.
XX
AC ABU47877;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #33404.
XX
DE Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS *Salmonella typhi*.
XX
PN WO20027183-A2.
XX
PD 03-OCT-2002.
XX
PE 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haeselbeck R, Ohlsen KL, Zykkind JW;
PI Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA51747..
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 75801; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 367 AA:
Query Match 66.7%; Score 44; DB 6; Length 367;
Best Local Similarity 69.2%; Pred. No. 48;
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
Qy 1 GPMELV---GYF 9
Db 127 GPMELVLPFGYF 139
RESULT 5
ADH12894
ID ADH12894 standard; protein; 207 AA.
XX
AC ADH12894;
XX
DT 25-MAR-2004 (first entry)
XX
DE *Francisella tularensis* immunogenic protein 75, SEQ ID NO:75.
XX
DE Immunogenic protein; protective immune response; vaccine;
XX
OS *Francisella tularensis*.

XX WO2004003009-A2.
 PN 08-JAN-2004.
 PD 26-JUN-2003; 2003WO-GB002718.
 XX 28-JUN-2002; 2002GB-00014942.
 PR (MINA) UK SEC FOR DEFENCE.
 XX Titball RW, Mayers CN, Duffield ML, Miller J, Rowe SC.
 PI WPI; 2004-083016/08.
 DR N-PSDB; ADH12994.
 XX New protein, useful as a vaccine for producing a protective immune
 PT response in a mammal against infection by *Francisella tularensis*, or
 PT preventing or treating *Francisella tularensis* infection in a mammal.
 XX Claim 1; SEQ ID NO 75; 217pp; English.
 PS
 CC The invention relates to 100 potentially immunogenic proteins from
 CC *Francisella tularensis* (ADH12820-ADH12919) and nucleic acids encoding
 CC them (ADH12920-ADH13019) which may be used in vaccines. The nucleic acids
 CC may be contained within a vaccine, bacterial or plasmid vector. The
 CC invention also relates to a pharmaceutical composition comprising the
 CC protein or the nucleic acid in combination with a pharmaceutical carrier
 CC or excipient. The proteins and nucleic acids are useful in vaccine
 CC compositions for producing a protective immune response against
 CC *Francisella tularensis* infection in a mammal, or for preventing or
 CC treating *Francisella tularensis* infection in a mammal. The present
 CC sequence represents a *Francisella tularensis* protein of the invention.
 XX
 SQ Sequence 207 AA;

Query Match 65.2%; Score 43; DB 8; Length 207;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPMELVNG 7
 DB 120 GPMELVNG 126

RESULT 6
 ABM89125
 ID ABM89126 standard; protein; 415 AA.
 XX
 AC ABM89126;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DE Rice abiotic stress responsive polypeptide SEQ ID NO:7372.
 XX
 KW abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
 XX
 OS *Oryza sativa*.
 XX
 PN WO2003008540-A2.
 XX
 PD 30-JAN-2003.
 XX
 PF 21-JUN-2002; 2002WO-US019668.
 XX
 PR 22-JUN-2001; 2001US-0300112P.
 XX
 PR 24-AUG-2001; 2001US-0314662P.
 XX
 PR 26-SEP-2001; 2001US-0325277P.
 XX
 PR 21-NOV-2001; 2001US-0332132P.
 XX
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F,
 XX

PI Moughamer T, Provart N, Riche D, Zhu T,
 XX
 DR WPI; 2003-248011/24.
 XX
 PT New stress-responsive nucleic acid, useful for altering the
 PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
 PT stress, salt stress or osmotic stress.
 XX
 XX Claim 1; SEQ ID NO 7372; 89pp; English.
 PS
 CC The invention relates to novel abiotic stress responsive polynucleotides
 CC and polypeptides. Also disclosed are vectors, expression cassettes, host
 CC cells, and plants containing such polynucleotides. Also disclosed are
 CC methods for using the polynucleotides and polypeptides to alter the
 CC responsiveness of a plant to abiotic stress. The invention is useful in
 CC agriculture. The nucleic acid is useful for determining whether a test
 CC plant has been exposed to an abiotic stress condition. It is also useful
 CC for selecting an agent that alters abiotic stress regulated
 CC polynucleotide expression in a plant cell, and to identify a homolog or
 CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
 CC molecule and the polypeptide encoded by it are useful in altering the
 CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
 CC stress, osmotic stress or any of their combinations. The present sequence
 CC is used in the exemplification of the invention
 XX
 SQ Sequence 415 AA;

Query Match 63.6%; Score 42; DB 7; Length 415;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GPMELVNG 8
 DB 176 GPMELVNG 183

RESULT 7
 AA008773
 ID AA008773 standard; protein; 114 AA.
 XX
 AC AA008773;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 22665.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX
 OS *Homo sapiens*.
 XX
 PN WO200164835-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-US004927.
 XX
 PR 28-FEB-2000; 2000US-00515126.
 XX
 PR 18-MAY-2000; 2000US-00577409.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-514838/56.
 XX
 DR N-PSDB; AA188704.
 XX
 PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.
 XX
 PS Claim 20; SEQ ID NO 22665; 1399pp + Sequence Listing; English.
 XX

XX The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX

SO Sequence 114 AA;

Query Match 62.1%; Score 41; DB 4; Length 114;
Best Local Similarity 55.6%; Pred. No. 46;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVGYF 9
|||:|:|:
Db 76 GPMKFLGFF 84

RESULT 8
AAR88504

ID AAR88504 standard; protein; 121 AA.

XX AAR88504;

XX 31-JUN-1996 (first entry)

XX Vhm for antibody BT34/A5.

XX Antibody; variable heavy chain; Vhm; human; monoclonal; Mab; BT34/A5;

XX BT32/A6; cell cycle independent; tumour specific; glioma; therapy;

XX detection; complementarity determining region; CDR.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 31..35 /note="complementarity determining region (specifically
FT claimed)"

XX Region 50..66 /note="complementarity determining region (specifically
FT claimed)"

XX Region 99..110 /note="complementarity determining region (specifically
FT claimed)"

XX Region 99..110 /note="complementarity determining region (specifically
FT claimed)"

XX WO9535374-A1.

XX 28-DEC-1995.

XX 16-JUN-1995; 95WO-CA000361.

XX 21-JUN-1994; 94US-00264093.

XX (DANM/) DAN M D.

XX Dan MD;

XX WPI; 1996-058411/06.

XX N-PSDB; AAT10938.

XX Novel monoclonal antibodies, BT34/A5 and BT32/A6 - used to characterise
XX glioma specific cell surface antigens, and in the treatment of glioma.

XX Claim 8; Page 33; 53pp; English.

CC AAR88504-R88510 represent regions of the human monoclonal antibodies
CC (Mab's) BT34/A5 and BT32/A6. This sequence represents the variable region
CC of the heavy chain, subgroup mu, (Vhm) of BT34/A5. The complementarity
CC determining regions (CDR's) of this sequence are specifically claimed.
CC This sequence preferably has an N-terminal extension comprising the
CC signal sequence represented in AAR88505. The BT34/A5 and BT32/A6 Mab's
CC recognise a cell cycle independent tumour specific antigen. They also
CC bind equally well to tumour cells in vitro regardless of their culture
CC viability, growth characteristics, or culture density. The antibodies
CC effectively label the tumour cells by binding to the antigen present on
CC the cell surface. The Mab's are useful in the detection and the treatment
CC of glioma. These Mab's are specific for glioma and show none of the cross
CC reactivity seen with previous antibodies
XX

SO Sequence 121 AA;

Query Match 62.1%; Score 41; DB 2; Length 121;
Best Local Similarity 60.0%; Pred. No. 49;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPMELVGYFD 10
|||:|:|:
Db 100 GWMDLNVPD 109

RESULT 9
ABU20453

ID ABU20453 standard; protein; 475 AA.

XX ABU20453;

XX 19-JUN-2003 (first entry)

XX Protein encoded by prokaryotic essential gene #5980.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Bacterioides fragilis.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00672851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX N-PSDB; ACA24323.

XX Claim 25; SEQ ID NO 48377; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation, or to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 CC Sequence 475 AA;

Query Match 62.1%; Score 41; DB 6; Length 475;
 Best Local Similarity 54.5%; Pred. No. 2.1e+02;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPMELVGFDS 11
 Db 404 GDMKLIYYDS 414

RESULT 10

ADC07986 ADC07986 standard; protein; 792 AA.

AC ADC07986;

DT 18-DEC-2003 (first entry)

DE Rice protein sequence Seq ID252 related to grain filling.

XX plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 XX carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
 KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
 KW gene; ds; plant.

OS *Oryza sativa*.

PN MO2003000905-A2.

PD 03-JAN-2003.

PF 21-JUN-2002; 2002WO-1B002450.

PR 22-JUN-2001; 2001US-0300112P.

PR 26-SEP-2001; 2001US-0325277P.

PR 20-DEC-2001; 2001US-0342327P.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

PI Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
 PI Glazebrook J, Katagiri F, Kreps J, Provart N, Ricke D;

DR MPI; 2003-229341/22.

DR N-PSDB; ADC07985.

PT New plant genes encoding polypeptides having an activity involved in or
 associated with the synthesis, metabolism or degradation of carbohydrates

PT in the plant grain useful in generating plants having improved
 PT nutritional properties.

PS Claim 23; SEQ ID NO 252; 130bp; English.

CC This invention, in the area of plant biotechnology, relates to novel
 CC polynucleotides comprising a nucleotide sequence encoding a protein which
 CC is involved in or associated with the synthesis, metabolism or
 CC degradation of carbohydrates in the plant grain and the expression of
 CC which is up-regulated during grain filling. The plant is selected from
 CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
 CC sugarbeet, wheat, and rice. The invention may be useful for the
 CC improvement of protein, oil, starch, fibre and moisture content of the
 CC cereal grains. In addition, carbohydrate levels may be modified to a more
 CC desirable level using the present invention. The present sequence is the
 CC amino acid sequence of a rice protein of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences.

CC Sequence 792 AA;

Query Match 62.1%; Score 41; DB 7; Length 792;
 Best Local Similarity 66.7%; Pred. No. 3.6e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PMELVGFYD 10
 Db 245 PMQLGYGD 253

RESULT 11

ABB67542 ABB67542 standard; protein; 1352 AA.

AC ABB67542;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 29418.

DE Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.

OS *Drosophila melanogaster*.

PN MO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US0009231.

PR 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.

PA (PEKE) PB CORP NY.

PI Venter JC, Adams M, Li PWD, Myers BW;

DR MPI; 2001-656860/75.

DR N-PSDB; ABB11645.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from *Drosophila* and for elucidating cell signaling and cell-cell
 PT interactions.

PS Disclosure; SEQ ID NO 29418; 21bp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from *Drosophila*. The invention is
 CC useful in developmental biology and in elucidating cell signaling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins (AB557737-
CC AB572072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1352 AA;

Query Match 62.1%; Score 41; DB 4; Length 1352;
Best Local Similarity 77.8%; Pred. No. 6.3e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 2;

Qy 3 WELVGYFDS 11
Db 161 WRNNGYFDS 169

RESULT 12
ABP56656
ID ABP56656 standard; protein; 146 AA.
XX
AC ABP56656;
XX
DT 25-MAR-2003 (first entry)
XX
DE Chimpanzee C68 adenovirus E3 16 kDa protein SEQ ID NO:21.
XX
KW Chimpanzee C68 adenovirus; rapid screening; bacterial transformant;
KW simian adenovirus; cytostatic; antiproliferative; antitumoral; vaccine;
KW adenoviral; capsid protein; hexon; penton; fibre protein; cancer;
KW hyperproliferative condition; psoriasis; infection.
XX
OS Mastadenovirus.

XX
FH Key Location/Qualifiers
FT Misc-difference 62
FT note="any amino acid"

XX
PN WO200300851-A2.

XX
PD 03-JAN-2003.

XX
PF 20-JUN-2002; 2002WO-US019735.

XX
PR 22-JUN-2001; 2001US-0300501P.

XX
PR 04-JUN-2002; 2002US-0385632P.

XX
PA (UYPB-) UNIV PENNSYLVANIA.

XX
PI Gao G, Wilson JM;

XX
DR WPI; 2003-184043/18.

XX
DR N-PSDB; ABZ22473.

XX
PT New C68 chimpanzee adenoviral capsid protein, useful for preparing a
PT composition for treating hyperproliferative conditions e.g., cancer or
PT psoriasis and as a vaccine against bacterial, fungal, viral or parasitic
PT infection.

XX
PS Disclosure; Page 88; 124pp; English.

XX
XX The present invention describes a chimpanzee C68 adenoviral capsid
CC protein, which is substantially free of other viral proteins with which
CC it is naturally associated, comprising: (a) a hexon protein comprising
CC 514-amino acid sequence (see ABP56652); (b) a penton protein comprising
CC 534-amino acid sequence (see ABP56647); (c) a fibre protein comprising
CC 425-amino acid sequence (see ABP56662); or (d) a unique fragment of any
CC of (A)-(C) comprising 8-amino acid residues in length. Also described:
CC (1) a novel adenovirus serotype comprising a unique fragment of the C68
CC hexon protein fused to a heterologous adenovirus hexon peptide; (2) a
CC recombinant or pseudotyped adenovirus comprising a capsid of the novel
CC adenovirus serotype encapsidating a molecule for delivery to a target
CC cell; (3) an adenoviral capsid; (4) a pharmaceutical composition; (5)

CC rapid screening of recombinant constructs; and (6) a host cell. The
CC chimpanzee C68 adenoviral capsid protein has cytostatic, antiproliferative
CC and antimicrobial activities, and can be used in vaccines. The chimpanzee
CC C68 adenoviral capsid protein is useful for preparing a composition for
CC treating hyperproliferative conditions e.g., cancer or psoriasis and as a
CC vaccine against bacterial, fungal, viral or parasitic infection. The
CC present sequence represents a chimpanzee C68 adenovirus E3 16 kDa
CC protein, which is given in the exemplification of the present invention
XX
SQ Sequence 146 AA;

Query Match 60.6%; Score 40; DB 6; Length 146;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPWELVG 7
Db 101 GPWEVVG 107

RESULT 13
ABM70292
ID ABM70292 standard; protein; 283 AA.
XX
AC ABM70292;
XX
DT 20-NOV-2003 (first entry)
XX
DE Photobhabdus luminescens protein sequence #3389.

XX
DE Photobhabdus luminescens protein sequence #3389.
XX
KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
KW detection; food; gene expression; plant; animal; microorganism; toxin;
KW antibiotic; biopesticide; virulence factor; disease model; plague;
KW whooping cough.

XX
OS Photobhabdus luminescens.

XX
PN WO200294867-A2.

XX
PD 28-NOV-2002.

XX
PF 07-FEB-2002; 2002WO-IB003040.

XX
PR 07-FEB-2001; 2001FR-00001659.

XX
PA (INSP) INST PASTEUR.

XX
PA (CNRS) CNRS CENT NAT RECH SCI.

XX
PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
PI Buchrieser C;

XX
DR WPI; 2003-148459/14.

XX
PT Genomic sequence of Photobhabdus luminescens and encoded polypeptides,
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.
XX
PS Claim 2; SEQ ID NO 3389; 1205pp; French.

XX
XX The invention relates to the isolation of genes and their encoded
CC proteins from Photobhabdus luminescens. The isolated sequences are
CC sources of probes and primers for detecting the genome of P. luminescens
CC and related species; to study polymorphisms; for gene analysis and for
CC detection/amplification of the genes. Antibodies (Ab) raised against the
CC polypeptides encoded by the genes are used for detection/identification
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than P. luminescens and are able to alter
CC response or sensitivity to toxins and antibiotics produced by P.
CC luminescens. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful

CC therapeutically (to treat microbial infection by bacteria or fungi that
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
CC biopesticides. Other uses of the genes and the proteins are as virulence
CC factors and for identifying targets of human diseases for which P.
CC luminescens is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated P. luminescens proteins

XX SQ Sequence 283 AA;

Query Match 60.6%; Score 40; DB 6; Length 283;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 WELVGYFDS 11
Db 238 WLIVGYFDA 246

RESULT 14
ADY22314
ID ADY22314 standard; protein; 477 AA.

XX AC ADY22314;

XX DT 21-APR-2005 (first entry)

XX DE Plant full length insert polypeptide seqid 70098.

XX KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content.

XX OS Unidentified.

XX PN US2004034888-A1.

XX PD 19-FEB-2004.

XX PF 28-APR-2003; 2003US-00425114.

XX PR 06-MAY-1999; 99US-00304517.

XX PR 05-NOV-2001; 2001US-00985678.

XX PA (LIUJ/) LIU J.

XX PA (ZHOU/) ZHOU Y.

XX PA (KOVA/) KOVALIC D K.

XX PA (SCRE/) SCREEN S B.

XX PA (TABAS/) TABASKA J E.

XX PA (CAOY/) CAO Y.

XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;

XX DR WPI; 2004-180133/17.

XX PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.

XX PS Claim 1, SEQ ID NO 70098; 15pp; English.

XX CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme

CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.

XX SQ Sequence 477 AA;

Query Match 60.6%; Score 40; DB 8; Length 477;
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPMELVGYFD 10
Db 307 GPMEMREFD 316

RESULT 15
AAG32050

ID AAG32050 standard; protein; 885 AA.

XX AC AAG32050;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 38593.

XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

XX PR 09-MAR-1999; 99US-0123180P.

XX PR 23-MAR-1999; 99US-0123548P.

XX PR 25-MAR-1999; 99US-0125788P.

XX PR 29-MAR-1999; 99US-0126264P.

XX PR 01-APR-1999; 99US-0126785P.

XX PR 06-APR-1999; 99US-0127462P.

XX PR 08-APR-1999; 99US-0128714P.

XX PR 16-APR-1999; 99US-0128845P.

XX PR 19-APR-1999; 99US-0130077P.

XX PR 21-APR-1999; 99US-0130451P.

XX PR 23-APR-1999; 99US-0130510P.

XX PR 28-APR-1999; 99US-0130891P.

XX PR 30-APR-1999; 99US-0132048P.

XX PR 04-MAY-1999; 99US-0132407P.

XX PR 05-MAY-1999; 99US-0132484P.

XX PR 06-MAY-1999; 99US-0132485P.

XX PR 07-MAY-1999; 99US-0132486P.

XX PR 11-MAY-1999; 99US-0132863P.

XX PR 14-MAY-1999; 99US-0134256P.

XX PR 14-MAY-1999; 99US-0134218P.

XX PR 14-MAY-1999; 99US-0134219P.

XX PR 14-MAY-1999; 99US-0134370P.

XX PR 18-MAY-1999; 99US-0134768P.

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PR 31-AUG-1999; 99US-0151438P.
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PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
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PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.

PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 60.6%; Score 40; DB 3; Length 885;
Best Local Similarity 85.7%; Pred.No. 6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPMELVG 7
||:|
Db 411 GPMOLVG 417

Search completed: December 4, 2005, 04:44:57
Job time : 98.5625 secs

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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:45 ; Search time 15.5833 Seconds
(without alignments)
67.918 Million cell updates/sec

Title: US-10-632-706-128
Perfect score: 66
Sequence: 1 GPMELVGYFDS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	44	66.7	367	2	AD0922
3	43	65.2	1788	2	T29043
4	41	62.1	491	2	E69368
5	41	62.1	550	2	B84900
6	41	62.1	619	1	S48729
7	41	62.1	697	2	G70704
8	40	60.6	724	2	B87015
9	40	60.6	726	2	T44905
10	40	60.6	888	2	D84824
11	40	60.6	931	2	F84637
12	39	59.1	299	2	D71051
13	39	58.1	320	2	T33303
14	39	59.1	459	2	S17907
15	39	59.1	471	2	S28476
16	39	59.1	578	2	B82204
17	39	59.1	949	1	PKMUP1
18	38	57.6	173	2	C74403
19	38	57.6	274	2	C75335
20	38	57.6	409	2	S63614
21	38	57.6	432	2	T17829
22	38	57.6	465	2	T26146
23	38	57.6	496	2	G71693
24	38	57.6	499	2	G97761
25	38	57.6	532	2	AP3498
26	38	57.6	1091	2	T34247
27	38	57.6	1107	2	T34246
28	38	57.6	2100	2	T03223
29	37	56.1	213	2	C64041

30	37	56.1	217	2	A82491	fine protein VCA01
31	37	56.1	226	2	A87664	hypothetical prote
32	37	56.1	235	2	T44679	spou protein homol
33	37	56.1	241	2	T39330	probable 60S acid
34	37	56.1	276	2	A95309	probable ABC trans
35	37	56.1	277	2	AF3216	ABC transporter, m
36	37	56.1	349	2	T31856	hypothetical prote
37	37	56.1	365	2	S61636	hypothetical prote
38	37	56.1	400	2	AF0291	probable drug resi
39	37	56.1	413	2	G95965	conserved hypothet
40	37	56.1	426	2	T08550	choleline monooxygen
41	37	56.1	462	2	I58179	5HT3 receptor subu
42	37	56.1	468	2	T48615	hypothetical prote
43	37	56.1	502	2	S50519	hypothetical prote
44	37	56.1	601	1	A64222	heat shock protein
45	37	56.1	642	2	G69371	acetyl-CoA synthet

ALIGNMENTS

RESULT 1

T35791
probable transmembrane sugar transport protein - Streptomyces coelicolor
C.Species: Streptomyces coelicolor
C.Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C.Accession: T35791
R.Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1998
A.Reference number: Z21570
A.Accession: T35791
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-279 <SER>
A.Cross-references: UNIPROT:O87858; UNIPARC:UPI00000DAC47; EMBL:AL031013; PIDD:CAA19796.
A.Experimental source: strain A3(2)
C.Genetics:
A.Gene: SCOEDB:SC8A6.24
C.Superfamily: maltose transport protein malG

Query Match 68.2%; Score 45; DB 2; Length 279;
Best Local Similarity 77.8%; Pred. No. 2.8;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 MELVGYFDS 11
DB 160 WMLGYFDS 168

RESULT 2

AD0922
Probable undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase STY3637 (imported)
C.Species: Salmonella enterica subsp. enterica serovar Typhi
A.Note: this species has also been called Salmonella typhi
C.Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 03-Feb-2003
C.Accession: AD0922
R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Parkhill, J.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001
A.Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A.Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A.Reference number: AB0502; MUID:21534947; PMID:11677608
A.Accession: AD0922

A.Molecule type: DNA
A.Status: preliminary
A.Residues: 1-367 <PAR>
A.Cross-references: UNIPARC:UPI000005A58F; GB:AL513382; PIDD:CAD09398.1; PIDD:g16504516;
C.Genetics:
A.Gene: STY3637

Query Match 66.7%; Score 44; DB 2; Length 367;
Best Local Similarity 69.2%; Pred. No. 5.6;

Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
Qy 1 GPMELVYGF 9
|||
|||
Db 127 GPMELVLPFGYF 139

RESULT 3

T29043
hypothetical protein B0228.2 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T29043
R:Leimach, D.
Submitted to the EMBL Data Library, March 1995
A:Description: The sequence of C. elegans cosmid B0228.
A:Reference number: Z18324
A:Accession: T29043
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1788 <LEI>
A:Cross-references: UNIPROT:O81G61; UNIPARC:UPI00000851C9; EMBL:U23168; PIDN:AAC38806.1;
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CBSP:B0228.2
A:Introns: 1456/2; 1482/3; 1516/2; 1551/3; 1595/3; 1646/1; 1671/1; 1716/2; 1749/3

Query Match 65.2%; Score 43; DB 2; Length 1788;
Best Local Similarity 60.0%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPMELVGYFD 10
|||
|||
Db 1722 GPMNMGGRFD 1731

RESULT 4

B69368
glutamine synthetase (gluA) homolog - *Archaeoglobus fulgidus*
C:Species: *Archaeoglobus fulgidus*
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: B69368
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirschner, B.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uitterlinden, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Moese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: B69368
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-491 <KLB>
A:Cross-references: UNIPROT:Q29313; UNIPARC:UPI0000056F0D; GB:AE001039; GB:AE000782; NID
C:Superfamily: glutamate-ammonia ligase

Query Match 62.1%; Score 41; DB 2; Length 491;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PWEVLGYFD 10
|||
|||
Db 482 PWEFMKYFD 490

RESULT 5

B84900
hypothetical protein At2g46220 [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: B84900
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Mayan, L.; Tallon, L.;
euser, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A:Reference number: A84420; MUID:20883487; PMID:10617197
A:Accession: B84900
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-550 <STO>
A:Cross-references: UNIPROT:O82347; UNIPARC:UPI000017A71B; GB:AE002093; NID:G3702327; PII
C:Genetics:
A:Gene: At2g46220
A:Map position: 2

Query Match 62.1%; Score 41; DB 2; Length 550;
Best Local Similarity 70.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPMELVGYFD 10
|||
|||
Db 176 GPMSTRGRFD 185

RESULT 6

S48729
glucokinase regulator - African clawed frog
C:Species: *Xenopus laevis* (African clawed frog)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S48729; S49339
R:Veiga-da-Cunha, M.; Delvaux, M.; Watelet, N.; van Schaftingen, E.
Eur. J. Biochem. 225, 43-51, 1994
A:Title: Cloning and expression of a *Xenopus* liver cDNA encoding a fructose-phosphate-in
A:Reference number: S48729; MUID:95010134; PMID:7925465
A:Accession: S48729
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-619 <VEI>
A:Cross-references: UNIPROT:Q91754; UNIPARC:UPI000012B2E2; EMBL:X80901; NID:G556677; PII
C:Superfamily: glucokinase regulator

Query Match 62.1%; Score 41; DB 1; Length 619;
Best Local Similarity 63.6%; Pred. No. 32;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GPMELVGYFDS 11
|||
|||
Db 17 GPMELVGYFDS 27

RESULT 7

G70704
hypothetical protein RV2326C - *Mycobacterium tuberculosis* (strain H37RV)
C:Species: *Mycobacterium tuberculosis*
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: G70704
R:Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
J.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sultson, J.E.; Taylor, K.; Whithead, S.; Barrett, B.G.
A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: G70704
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-697 <COL>
A:Cross-references: UNIPROT:P71886; UNIPARC:UPI000013BA74; GB:Z79702; GB:AL123456; NID:G
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: RV2326C

Query Match 62.1%; Score 41; DB 2; Length 697;
Best Local Similarity 66.7%; Pred. No. 36;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Oy 2 PMELVGYD 10
 |||:||||
 Db 196 PMVLGGYFN 204

RESULT 8

B87015

ABC transporter ML0848 [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C:Accession: B87015

R: Cole, S.T.; Sigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; He

am, M.A.; Rutherford, K.M.; Davies, R.M.; Devlin, K.; Duthey, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

Nature 409, 1007-1011, 2001

A: Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S

A: Title: Massive gene decay in the leprosy bacillus.

A: Reference number: A86909; MUID:21128732; PMID:11234002

A: Accession: B87015

A: Status: preliminary

A: Molecule type: DNA

A: Residues: 1-724 <STO>

A: Cross-references: UNIPROT:Q9CCF9; UNIPARC:UPI00000C6D27; GB:AL450380; NID:g13092926; F

C: Genetics:

A: Gene: ML0848

Query Match

Best Local Similarity 60.6%; Score 40; DB 2; Length 724;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 2 PMELVGYF 9
|||:||||

Db 224 PMVLGGYF 231

RESULT 9

T44905

ABC-type transporter homolog [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004

C:Accession: T44905

R: Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1997

A: Reference number: Z22864

A: Accession: T44905

A: Status: preliminary; translated from GB/EMBL/DBJ

A: Molecule type: DNA

A: Residues: 1-726 <PAR>

A: Cross-references: UNIPROT:O32971; UNIPARC:UPI00000BDD0E; EMBL:Z98741; PIDN: CAB11403.1

C: Genetics:

A: Experimental source: cosmid B22

A: Note: MLCB22.38c

Query Match

Best Local Similarity 60.6%; Score 40; DB 2; Length 726;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 2 PMELVGYF 9
|||:||||

Db 226 PMVLGGYF 233

RESULT 10

D84824

probable DNA-directed RNA polymerase II subunit [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: D84824

R: Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanKen, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eilen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A: Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A: Reference number: A84420; MUID:20083487; PMID:10617197

A: Accession: D84824

A: Status: preliminary

A: Molecule type: DNA

A: Residues: 1-888 <STO>

A: Cross-references: UNIPROT:O04206; UNIPARC:UPI00000A517F; GB:AE002093; NID:g2088656; PI

C: Genetics:

A: Gene: At2g40030

A: Map position: 2

Query Match

Best Local Similarity 60.6%; Score 40; DB 2; Length 888;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GPMELVGYFDS 11
|||:||||

Db 544 GPMELVGYFDS 554

RESULT 11

F84637

probable plasma membrane proton ATPase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004

C:Accession: F84637

R: Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanKen, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eilen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A: Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A: Reference number: A84420; MUID:20083487; PMID:10617197

A: Accession: F84637

A: Status: preliminary

A: Molecule type: DNA

A: Residues: 1-931 <STO>

A: Cross-references: UNIPARC:UPI000016237B; GB:AE002093; NID:g4572678; PIDN: AAD23893.1; G

C: Genetics:

A: Gene: At2g24520

A: Map position: 2

C: Superfamily: Na(+)/K(+) -transporting ATPase alpha chain; ATPase nucleotide-binding dome

Query Match

Best Local Similarity 60.6%; Score 40; DB 2; Length 931;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPMELVGY 7
|||:||||

Db 457 GPMQVLGY 463

RESULT 12

D71051

hypothetical protein PH1107 - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 31-Dec-2004

C:Accession: D71051

R: Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin

M.; Ohtuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi

DNA Res. 5, 55-76, 1998

A: Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a

A: Reference number: A71000; MUID:98344137; PMID:9679194

A: Accession: D71051

A: Status: preliminary; nucleic acid sequence not shown; translation not shown

A: Molecule type: DNA

A: Residues: 1-299 <KAW>

A: Cross-references: UNIPROT:O58834; UNIPARC:UPI0000062FB7; GB:AP000005; NID:g3236132; PI

A: Experimental source: strain OT3

A: Note: this accession replaces an interim accession for a sequence replaced by GenBank

C: Genetics:

A: Gene: PH1107

C: Superfamily: glycosidase, PH1107 type

Query Match 59.1%; Score 39; DB 2; Length 299;
 Best Local Similarity 60.0%; Pred. No. 33;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PWELVGYFDS 11
 |||||
 Db 247 PWELGHWND 256

RESULT 13

hypothetical protein R01B10.4 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C:Accession: T33303

R:Langston, Y.; Beck, C.

submitted to the EMBL Data Library, May 1998

A:Description: The sequence of *C. elegans* cosmid R01B10.

A:Reference number: 221318

A:Accession: T33303

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-320 <LAN>

A:Cross-references: UNIPROT:O61975; UNIPARC:UPI0000080228; EMBL:AF068718; PIDD:AACT7768.

A:Experimental source: strain Bristol N2; clone R01B10

C:Genetics:

A:Gene: CESP:R01B10.4

A:Map position: 5

A:introns: 25/2; 73/2; 211/3; 241/2

Query Match 59.1%; Score 39; DB 2; Length 320;
 Best Local Similarity 55.6%; Pred. No. 36;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 WELVGYFDS 11
 |||||
 Db 65 WDTIGHFDS 73

RESULT 14

glutamate dehydrogenase (NADP) (EC 1.4.1.4) - yeast (*Schwanniomyces occidentalis* var. oc

C:Species: *Schwanniomyces occidentalis* var. *occidentalis*

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Oct-2004

C:Accession: S17907

R:de Zoysa, P.A.; Connerton, I.F.; Watson, D.C.; Johnston, J.R.

Curr. Genet. 20, 219-224, 1991

A:Title: Cloning, sequencing and expression of the *Schwanniomyces occidentalis* NADP-depe

A:Reference number: S17907; MUID:92035089; PMID:1934128

A:Accession: S17907

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-459 <DEZ>

A:Cross-references: UNIPROT:P29507; UNIPARC:UPI00001292F9

C:Superfamily: glutamate dehydrogenase

C:Keywords: NADP; oxidoreductase

Query Match 59.1%; Score 39; DB 2; Length 459;
 Best Local Similarity 66.7%; Pred. No. 52;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PWELVGYFDS 10
 |||||
 Db 308 PMAKVGHFD 316

RESULT 15

S28476

rtBL protein VC0249 [similarity] - *Vibrio cholerae* (strain N16961 serogroup O1)

C:Species: *Vibrio cholerae*

C>Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004

C:Accession: S28476; H82346

R:Manning, P.A.
 submitted to the EMBL Data Library, May 1991

A:Reference number: S28467

A:Accession: S28476

A:Molecule type: DNA

A:Residues: 1-471 <MAN>

A:Cross-references: UNIPROT:Q06959; UNIPARC:UPI00000D470B; EMBL:X59554; NID:g48381; PIDD:

A:Experimental source: strain O17

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;

Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dreger, I.; Sellers, P.

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 405, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: H82346

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-471 <HEI>

A:Cross-references: UNIPARC:UPI00000D470B; GB:AE004113; GB:AE003852; NID:g9654648; PIDD:

A:Experimental source: serogroup O1; strain N16961; biotype El tor

C:Genetics:

A:Gene: rfbV; VC0249

C:Superfamily: 4-connarate-CoA ligase; acetate-CoA ligase homology

F:47-468/Domain: acetate-CoA ligase homology <ACT>

Query Match 59.1%; Score 39; DB 2; Length 471;
 Best Local Similarity 60.0%; Pred. No. 54;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PWELVGYFDS 11
 |||||
 Db 329 PMLDGYFEN 338

Search completed: December 4, 2005, 04:53:34
 Job time : 17.5833 secs

Query No.	Score	Query	Length	DB	ID	Description
1	45	68.2	279	2	087858_STRCO	087858 streptomycc
2	45	68.2	290	2	082m58_STRAW	082m58 streptomycc
3	45	68.2	748	2	OSN032_ZYMMO	OSnq32 zymomonas t
4	44	66.7	367	1	MECA_SALT1	082366 salmonella
5	44	66.7	367	1	MECA_SALT1	091657 salmonella
6	44	66.7	367	2	OSPKK1_SALPA	OSpkk1 salmonella
7	44	66.7	449	2	063n53_BURPS	063n53 burkholder
8	43	65.2	231	2	04K719_PSEF5	04K719 pseudomonas
9	43	65.2	1201	2	Q7UYR6_RHOBA	Q7uyr6 rhodospiril
10	43	65.2	1633	1	YF74_CAEEL	090921 caenorhabd
11	43	65.2	7548	2	OSWRU1_CAEEL	OSwru1 caenorhabd
12	42	63.6	272	2	Q748S8_GHOSL	Q748s8 geobacter
13	42	63.6	381	2	06K1T5_ORYSA	06K1t5 oryza sati
14	42	63.6	454	2	08TUV9_METAC	08Tuv9 methanosaar
15	42	63.6	578	2	Q8D959_VIBVU	Q8d959 vibrio vili
16	42	63.6	578	2	Q7MLB3_VIBVU	Q7mlb3 vibrio vili
17	42	63.6	1275	2	Q8Q061_METMA	Q8q061 methanosaar
18	41	62.1	211	2	Q8KHK7_PSEAE	Q8khk7 pseudomonas
19	41	62.1	241	2	082347_ABA7H	082347 arabidopsis1
20	41	62.1	273	2	Q7UND8_RHOBA	Q7und8 rhodospiril
21	41	62.1	318	2	Q4KEF0_PSEF5	Q4kef0 pseudomonas
22	41	62.1	491	1	GINA_ARCPU	029313 archaeoglo
23	41	62.1	518	2	OSLH40_BACFN	051140 bacteroides
24	41	62.1	518	2	Q64XZ7_BACFR	Q64xz7 bacteroides
25	41	62.1	613	1	Q6BTL3_DBBHA	Q6btl3 debaryomycc
26	41	62.1	619	1	CCKR_XENIA	091753 xenopus la
27	41	62.1	619	2	OSSKA5_THET8	OSska5 thermus th
28	41	62.1	619	2	Q6PAX3_XENLA	Q6pax3 xenopus la
29	41	62.1	697	1	Y2335_MYCTO	Y2335 mycobacter
30	41	62.1	697	1	Y2335_MYCTO	P63400 mycobacter
31	41	62.1	1350	2	Q9V5J7_DROME	Q9v5j7 drosophila

45	60.6	392	2	Q8LR17	PETHY
44	60.6	323	3	Q4INB2	GIBZE
43	60.6	319	2	Q4FPM2	PESMS
42	60.6	304	2	Q8TXO4	PESMS
41	60.6	282	2	Q7W9M4	PIOL
40	60.6	210	2	Q6BEL6	ADE04
39	60.6	39	2	Q6H1B6	9ADEN
38	60.6	208	2	Q6QPP9	9ADEN
37	60.6	207	2	Q6QPD3	9ADEN
36	60.6	206	2	Q6QP97	9ADEN
35	60.6	146	2	Q8UY74	9ADEN
34	60.6	122	2	Q8EB57	SHEON
33	62.1	2581	2	Q8W775	9YIRU
32	62.1	1370	2	Q7K0X6	BDOME
31	62.1	1170	2	Q7KXG6	DIOSPHILA
30	62.1	975	2	Q7C7K5	heterosigma
29	60.6	122	2	Q8EB57	shewanella
28	60.6	146	2	Q8UY74	simian aden
27	60.6	206	2	Q6QP97	simian aden
26	60.6	207	2	Q6QPD3	simian aden
25	60.6	208	2	Q6QPP9	simian aden
24	60.6	210	2	Q6H1B6	human aden
23	60.6	39	2	Q6BEL6	human aden
22	60.6	282	2	Q7W9M4	photorhabd
21	60.6	304	2	Q8TXO4	photorhabd
20	60.6	319	2	Q4FPM2	pseudomonas
19	60.6	323	3	Q4INB2	gibberella
18	60.6	392	2	Q8LR17	petunia hyb

ALIGNMENTS

RESULT 1	087858_STRCO	PRELIMINARY;	PRT;	279_AA.
ID	087858_STRCO	PRELIMINARY;	PRT;	279_AA.
AC	087858;			
DT	01-NOV-1998 (TRMBLrel. 08, Created)			
DT	01-NOV-1998 (TRMBLrel. 08, Last sequence update)			
DT	01-MAR-2004 (TRMBLrel. 26, Last annotation update)			
DE	Putative transmembrane sugar transport protein.			
GN	OrderedLocustNames=SCO6603; ORNames=SC8A6.24;			
OS	Streptomyces coelicolor.			
OC	Bacteria; Actinobacteriales; Actinobacteridae; Actinomycetales;			
OC	Streptomycinae; Streptomycetaceae; Streptomycetes.			
OX	NCBI_TaxID=1902;			
RA	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=A3(2) / M145;			
RX	MEBLIN=21996410; PubMed=12000953; DOI=10.1038/417141a;			
RA	Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,			
RA	Thompson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,			
RA	Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,			
RA	Cronin A., Fraser A., Goble A., Hiddaji J., Hornsby T., Howarth S.,			
RA	Huang C.-H., Kisser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,			
RA	Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,			
RA	Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,			
RA	Warren T., Wietzorek A., Woodward J.R., Barrell B.G., Parkhill J.,			
RA	Hopwood D.A.;			
RT	"Complete genome sequence of the model actinomycete Streptomyces			
RT	coelicolor A3(2).";			
RL	Nature 417:141-147(2002).			
CC	-1- FUNCTION: Part of a binding-protein-dependent transport system.			
CC	Probably responsible for the translocation of the substrate across			
CC	the membrane (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).			
CC	-1- SIMILARITY: Belongs to the binding-protein-dependent transport			
CC	system permease family.			
CC	EMBL; AL939128; CAA19796.1; -; Genomic_DNA.			
DR	PIR; T35791; T35791.			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	GO; GO:0005351; F:sugar porter activity; IEA.			
DR	GO; GO:0005215; F:transporter activity; IEA.			
DR	GO; GO:0006810; P:transport; IEA.			
DR	InterPro; IPR000515; BPD_transp_1; 1.			
DR	Pfam; PF00528; BPD_transp_1; 1.			
DR	PROSITE; PS00928; ABC_TM1; 1.			
KW	Complete proteome; Sugar transport; Transmembrane; Transport.			
SO	SEQUENCE 279 AA; 30335 MW; 886063385E853BPA CMC64;			
Query Match	68.2%;	Score 45;	DB 2;	Length 279;
Best Local Similarity	77.8%;	Pred. No. 25;		
Matches	7;	Conservative 1;	Mismatches 1;	Indels 0;
Gaps	0;			

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Db          160 WMLIGYFDS 168

RESULT 2
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Zymomonas.
OX NCBI_TaxID=542;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 31821 / ZM4 / GP4.
RX PubMed=15592456; DOI=10.1038/nbt1045;
RA Seo J.-S., Chong H., Park H.-S., Yoon K.-O., Jung C., Kim J.-J.,
RA Hong J.-H., Kim H., Kim J.-H., Kij J.-I., Park C.-J., Oh H.-M.,
RA Lee J.-S., Jin S.-J., Um H.-W., Lee H.-J., Oh S.-J., Kim J.-Y.,
RA Kang H.-L., Lee S.-Y., Lee K.-J., Kang H.-S.;
RT "The genome sequence of the ethanologenic bacterium Zymomonas mobilis
RT ZM4."
RL Nat. Biotechnol. 23:63-68(2005).
CC EMBL; AE008692; AAV89173.1; -; Genomic DNA.
DR GO; GO:0000175; F:3'-5'-exoribonuclease activity; IEA.
DR GO; GO:0004654; F:polynucleotide nucleotidyltransferase a. . .; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006356; P:RNA processing; IEA.
DR InterPro; IPR001247; 3 ExoRNase.
DR InterPro; IPR004088; KH_type_1.
DR InterPro; IPR012162; PNPase.
DR InterPro; IPR03029; S1.
DR Pfam; PF00013; KH_1; 1.
DR Pfam; PF03726; PNPase; 1.
DR Pfam; PF01138; RNase_PH; 2.
DR Pfam; PF03725; RNase_PH_C; 2.
DR Pfam; PF00575; S1; 1.
DR PIRSF; PIRSF005499; PNPase; 1.
DR SMART; SM00316; KH; 1.
DR SMART; SM00316; S1; 1.
DR PROSITE; PS50084; KH_TYPE_1; 1.
DR PROSITE; PS50126; S1; 1.
KW Complete proteome; Nucleotidyltransferase; Transferase.
SQ SEQUENCE 748 AA; 81949 MW; EB8C43821F85F6B CRC64;

Query Match          68.2%; Score 45; DB 2; Length 748;
Best Local Similarity 80.0%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY          2 PWELVGYFDS 11
DB          230 PWELVGYFDS 239

RESULT 4
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Zymomonas.
OX NCBI_TaxID=542;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CT18;
RX PubMed=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatista M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltham T., Hamlin N., Hague A., Hien T.T., Holroyd S., Jegerle K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gea P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,

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Db          160 WMLIGYFDS 168

RESULT 2
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Zymomonas.
OX NCBI_TaxID=542;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 31821 / ZM4 / GP4.
RX PubMed=15592456; DOI=10.1038/nbt1045;
RA Seo J.-S., Chong H., Park H.-S., Yoon K.-O., Jung C., Kim J.-J.,
RA Hong J.-H., Kim H., Kim J.-H., Kij J.-I., Park C.-J., Oh H.-M.,
RA Lee J.-S., Jin S.-J., Um H.-W., Lee H.-J., Oh S.-J., Kim J.-Y.,
RA Kang H.-L., Lee S.-Y., Lee K.-J., Kang H.-S.;
RT "The genome sequence of the ethanologenic bacterium Zymomonas mobilis
RT ZM4."
RL Nat. Biotechnol. 23:63-68(2005).
CC EMBL; AE008692; AAV89173.1; -; Genomic DNA.
DR GO; GO:0000175; F:3'-5'-exoribonuclease activity; IEA.
DR GO; GO:0004654; F:polynucleotide nucleotidyltransferase a. . .; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006356; P:RNA processing; IEA.
DR InterPro; IPR001247; 3 ExoRNase.
DR InterPro; IPR004088; KH_type_1.
DR InterPro; IPR012162; PNPase.
DR InterPro; IPR03029; S1.
DR Pfam; PF00013; KH_1; 1.
DR Pfam; PF03726; PNPase; 1.
DR Pfam; PF01138; RNase_PH; 2.
DR Pfam; PF03725; RNase_PH_C; 2.
DR Pfam; PF00575; S1; 1.
DR PIRSF; PIRSF005499; PNPase; 1.
DR SMART; SM00316; KH; 1.
DR SMART; SM00316; S1; 1.
DR PROSITE; PS50084; KH_TYPE_1; 1.
DR PROSITE; PS50126; S1; 1.
KW Complete proteome; Nucleotidyltransferase; Transferase.
SQ SEQUENCE 748 AA; 81949 MW; EB8C43821F85F6B CRC64;

Query Match          68.2%; Score 45; DB 2; Length 748;
Best Local Similarity 80.0%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY          2 PWELVGYFDS 11
DB          230 PWELVGYFDS 239

RESULT 4
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Zymomonas.
OX NCBI_TaxID=542;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CT18;
RX PubMed=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebatista M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltham T., Hamlin N., Hague A., Hien T.T., Holroyd S., Jegerle K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gea P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,

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RA Whitehead S., Barrrell B.G.:
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RX DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.:
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
CC -1- FUNCTION: Catalyzes the synthesis of Und-pp-GlcNAc (lipid I), the
CC first lipid-linked intermediate involved in ECA synthesis. This
CC lipid is also an acceptor for the addition of subsequent sugars to
CC complete the biosynthesis of O-antigen (By similarity).
CC -1- CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + undecaprenyl
CC phosphate = UMP + N-acetyl-alpha-D-glucosaminylidiphospho-
CC undecaprenol.
CC -1- COFACTOR: Magnesium and manganese (By similarity).
CC -1- PATHWAY: Synthesis of enterobacterial common antigen (ECA).
CC Synthesis of lipopolysaccharide O-antigen.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (By similarity).
CC -1- SIMILARITY: Belongs to the glycosyltransferase 4 family. Weca
CC subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL, AL637279; CAP09398.1; -; Genomic DNA.
DR EMBL, AE016845; AA070903.1; -; Genomic DNA.
DR InterPro; IPR0012750; ECA_Weca_rel.
DR InterPro; IPR000715; Glyco_trans_4.
DR Pfam; PF00953; Glycos_transf_4; 1.
DR TIGRfam; TIGR02380; ECA_weca_1.
KW Complete proteome; Glycosyltransferase; Inner membrane;
KW Lipopolysaccharide biosynthesis; Magnesium; Manganese; Membrane;
KW Transferrase; Transmembrane.
FT TRANSMEM 3 23 Potential.
FT TRANSMEM 45 65 Potential.
FT TRANSMEM 69 89 Potential.
FT TRANSMEM 106 126 Potential.
FT TRANSMEM 129 149 Potential.
FT TRANSMEM 158 178 Potential.
FT TRANSMEM 187 207 Potential.
FT TRANSMEM 213 233 Potential.
FT TRANSMEM 242 262 Potential.
FT TRANSMEM 294 314 Potential.
FT TRANSMEM 318 338 Potential.
SQ SEQUENCE 367 AA; 41086 MM; 28DA31CB1AE2D930 CRC64;
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Query Match 66.7%; Score 44; DB 1; Length 367;
Best Local Similarity 69.2%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
Oy 1 GPMELV-----GYF 9
Db 127 GPMELVLGPFQYF 139

RESULT 5
WECA_SALTY
ID WECA_SALTY STANDARD; PRT; 367 AA.
AC 0916R7; 033788;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)

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DE	Undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate transferase (EC 2.7.8.-) (UDP-GlcNAc:undecaprenyl-phosphate GlcNAc-1-phosphate transferase).
DE	Name=weca; Synonyms=rfe; OrderedLocusNames=STM3918; ORFNames=STMD1.72;
GN	Salmonella typhimurium.
OS	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC	Enterobacteriaceae; Salmonella.
OX	NCBI_TaxID=602;
RN	[1]
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC	STRAIN=LT12 / SCSG1412 / ATCC 700702.
RC	MEBLIN=21534948; PubMed=11677609; DOI=10.1038/35101614;
RC	McClelland M., Sanderson K.E., Spiehl J., Clifton S.W., Latreille P.,
RA	Courtney L., Portolillo S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA	Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA	Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA	Waterston R., Wilson R.K.;
RT	"Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.";
RL	Nature 413:852-856(2001).
RL	[2]
RP	NUCLEOTIDE SEQUENCE OF 111-367.
RP	STRAIN=LT12.
RC	MEBLIN=98409259; PubMed=9738879; DOI=10.1007/s004380050787;
RC	Modaillim C., Cano D.A., Casadeus J.;
RA	"The sfxX rfe and metN genes of Salmonella typhimurium and their
RT	involvement in the His(C) pleiotropic response.";
RL	Mol. Genet. 259:46-53(1998).
CC	-1- FUNCTION: Catalyzes the synthesis of Und-P-P-GlcNAc (lipid I), the
CC	first lipid-linked intermediate involved in ECA synthesis. This
CC	lipid is also an acceptor for the addition of subsequent sugars to
CC	complete the biosynthesis of O-antigen (By similarity).
CC	-1- CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + undecaprenyl
CC	phosphate = UMP + N-acetyl-alpha-D-glucosaminyl[diphospho-
CC	undecaprenol].
CC	-1- COFACTOR: Magnesium and manganese (By similarity).
CC	-1- ENZYME REGULATION: Inhibited by tunicamycin.
CC	-1- PATHWAY: Synthesis of enterobacterial common antigen (ECA).
CC	Synthesis of lipopolysaccharide O-antigen.
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC	(By similarity).
CC	-1- SIMILARITY: Belongs to the glycosyltransferase 4 family. WeCA
CC	subfamily.
CC	-----
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL collaboration -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use as long as its content is in no way modified and this statement is not
CC	removed.
CC	-----
DR	EMBL; AF233324; AAF3469.1; -; Genomic DNA.
DR	EMBL; AE008883; AL122767.1; -; Genomic DNA.
DR	EMBL; AJ002275; CAA05287.1; -; Genomic DNA.
DR	StyGene; SG7777; rfe.
DR	InterPro; IPR012750; ECA_weCA_rel.
DR	InterPro; IPR000715; Glyco_trans_4.
DR	Pfam; PF00953; Glycos_transf_1.
DR	TIGRfams; TIGR02380; ECA_weCA_1.
KW	Complete proteome; Glycosyltransferase; Inner membrane;
KW	Lipopolysaccharide biosynthesis; Magnesium; Manganese; Membrane;
KW	Transferrase; Transmembrane.
FT	TRANSMEM 3 23 Potential.
FT	TRANSMEM 45 65 Potential.
FT	TRANSMEM 69 89 Potential.
FT	TRANSMEM 106 126 Potential.
FT	TRANSMEM 129 149 Potential.
FT	TRANSMEM 158 178 Potential.
FT	TRANSMEM 187 207 Potential.
FT	TRANSMEM 213 233 Potential.
FT	TRANSMEM 242 262 Potential.
FT	TRANSMEM 294 314 Potential.
FT	TRANSMEM 318 338 Potential.
FT	CONFLICT 118 120 HLG -> ALS (in Ref. 2).

FT CONFLICT 128 138 PWEIVLGPFGY -> ALGVSAWPLMH (in Ref. 2).
 FT CONFLICT 146 148 MAA -> LNG (in Ref. 2).
 FT CONFLICT 220 S -> C (in Ref. 2).
 SQ SEQUENCE 367 AA; 41087 MM; IEDA31CB1AE2D938 CRC64;

Query Match 66.7%; Score 44; DB 1; Length 367;
 Best Local Similarity 69.2%; Pred. No. 49;
 Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 Oy 1 GPMELV---GYF 9
 Db 127 GPMELVLCGPGFY 139

RESULT 6
 OSEPK1 SALPA PRELIMINARY; PRT; 367 AA.

AC OSEPK1;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Putative undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase.
 GN Name: rfe; OrderedLocNames=SPA3758;
 OS Salmonella paratyphi-a.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=54388;

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ATCC 9150;
 RX PubMed=15531882; DOI=10.1038/ng1470;
 RA McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
 RA Porwollik S., Sabo A., Meyer R., Bieri T., Ozeraky P., McClelland M.,
 RA Harting C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
 RA Kohlberg S., Strong C., Du F., Carter J., Kremzki C., Layman D.,
 RA Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P.,
 RA Delhaunty K., Fronick C., Magrini V., Nhan M., Warren W., Florea L.,
 RA Splich J., Wilson R.K.;
 RT "Comparison of genome degradation in Paratyphi A and Typhi, human-restricted serovars of Salmonella enterica that cause typhoid";
 RL Nat. Genet. 36:1268-1274 (2004).
 DR EMBL; CP000026; AAV79540.1; -; Genomic DNA.
 DR GO; GO:0019866; C:inner membrane; IEA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016751; F:transferase activity; transferring glycosyl. . .; IEA.
 DR GO; GO:0006629; P:lipid metabolism; IEA.
 DR InterPro; IPR00715; Glyco_trans_4.
 DR pfam; PF00953; Glycosyltransferase; I2.
 DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN 1.
 KW Complete proteome; Glycosyltransferase; Transferase.
 SQ SEQUENCE 367 AA; 41086 MM; IEDA31CB1AE2D938 CRC64;

Query Match 66.7%; Score 44; DB 2; Length 367;
 Best Local Similarity 69.2%; Pred. No. 49;
 Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
 Oy 1 GPMELV---GYF 9
 Db 127 GPMELVLCGPGFY 139

RESULT 7
 O63N53 BURPS PRELIMINARY; PRT; 449 AA.

AC O63N53;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocNames=BPS0443;

OS Burkholderia pseudomallei (Pseudomonas pseudomallei).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia; pseudomallei group.
 OX NCBI_TaxID=28450;

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=K96243;
 RX PubMed=15377794; DOI=10.1073/pnas.0403302101;
 RA Holden M.T.G., Tildall R.W., Peacock S.J., Cerdeno-Tarrega A.-M.,
 RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
 RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
 RA Brooks K., Brown K.A., Brown N.P., Challis G.L., Cherevach I.,
 RA Chillingworth T., Cronin A., Crosscut B., Davis P., Desnazer D.,
 RA Felwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jasele K.,
 RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
 RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
 RA Songvilay S., Stevens K., Tumapa S., Vearatchaveest M.,
 RA Whitehead S., Yeats C., Barrett B.G., Oyston P.C.F., Parthill J.;
 RT "Genomic plasticity of the causative agent of melioidosis,
 Burkholderia pseudomallei.";
 RT Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245 (2004).
 DR EMBL; BX571966; CAH37899.1; -; Genomic DNA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 449 AA; 49531 MM; F1618B746D15240 CRC64;

Query Match 66.7%; Score 44; DB 2; Length 449;
 Best Local Similarity 75.0%; Pred. No. 60;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GPMELVGY 8
 Db 183 GPMRLIGY 190

RESULT 8

O4K719_PSEFS PRELIMINARY; PRT; 231 AA.

AC O4K719;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Phosphoserine phosphatase, putative.
 GN ORFNames=PFL4883;
 OS Pseudomonas fluorescens (strain Pf-5).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=220664;

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=PF-5;
 RX PubMed=15980661; DOI=10.1038/nbt1110;
 RA Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,
 RA Mavrodidi D., DeBoy R.T., Sehadri R., Ren Q., Madupu R., Dodson R.J.,
 RA Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,
 RA Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran J.,
 RA Khouli H.M., Pierson E., Pierson L., III, Thomasow L., Loper J.;
 RT "Complete genome sequence of the plant commensal Pseudomonas
 fluorescens Pf-5.";
 RL Nat. Biotechnol. 23:873-878 (2005).
 DR EMBL; CP000076; AAY94113.1; -; Genomic DNA.
 SQ SEQUENCE 231 AA; 25717 MM; A4DEA84C59107CF2 CRC64;

Query Match 65.2%; Score 43; DB 2; Length 231;
 Best Local Similarity 80.0%; Pred. No. 46;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 2 PWEIVGYFDS 11
 Db 61 PAELIGYFDS 70

RESULT 9
 Q7YRE_RHOBA

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ID Q7UYR6: RHODA PRELIMINARY; PRT; 1201 AA.
AC Q7UYR6;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocuNames=RB426;
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heilmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1."
RU Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294133; CAD71575.1; -; Genomic_DNA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:006118; P:electron transport; IEA.
DR InterPro; IPR012282; Cytochrome_c_R.
DR InterPro; IPR011429; PSC3.
DR Pfam; PF07635; PSCytl; 1.
DR Pfam; PF07583; PSCytl; 1.
DR Pfam; PF07587; PSD1; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1201 AA; 134482 MW; 728682735130D01 CRC64;

Query Match 65.2%; Score 43; DB 2; Length 1201;
Best Local Similarity 72.7%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GPMELVGYFDS 11
Db 1029 GLEWAVGYTDS 1039

RESULT 10
VP74 CAEEL STANDARD; PRT; 1633 AA.
ID VP74 CAEEL Q10908;
AC Q09221; Q10908;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Hypothetical protein B0228.4 in chromosome II.
GN ORFNames=B0228.4/B0228.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RT Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE REVISION.
RG Wormbase consortium;
RL Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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CC -----
CC EMBL; U23168; AAC38806.2; -; Genomic DNA.
DR Ensembl; B0228.4; Caenorhabditis elegans.
DR WormBase; WBGene0015061; B0228.4.
DR WormPep; B0228.4; CE31282.
DR InterPro; IPR010734; Copine.
DR Pfam; PF07002; Copine; 1.
DR PRINTS; PR00453; VMPADOMAIN.
KW Complete proteome; Hypothetical protein.
FT COMEBIAS 155 165 Cys-rich.
FT COMEBIAS 316 338 Lys-rich.
FT COMEBIAS 892 1019 Glu-rich.
SQ SEQUENCE 1633 AA; 183328 MW; 3B4EB46800B7A44D CRC64;

Query Match 65.2%; Score 43; DB 1; Length 1633;
Best Local Similarity 60.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPMELVGYFD 10
Db 1567 GPMWMMGRFD 1576

RESULT 11
Q5WRU1 CAEEL PRELIMINARY; PRT; 7548 AA.
ID Q5WRU1 CAEEL Q10908;
AC Q5WRU1 CAEEL Q10908;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Hypothetical protein B0228.4.
GN ORFNames=B0228.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RT Science 282:2012-2018(1998).
RU EMBL; U23168; AAU87832.1; -; Genomic DNA.
DR Ensembl; B0228.4; Caenorhabditis elegans.
DR WormBase; WBGene0015061; B0228.4.
DR WormPep; B0228.4; CE37470.
DR InterPro; IPR010734; Copine.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF07002; Copine; 1.
DR SMART; SM00327; VWA; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 7548 AA; 840584 MW; 8BEC3CC03D21C1C8 CRC64;

Query Match 65.2%; Score 43; DB 2; Length 7548;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPMELVGYFD 10
Db 7482 GPMWMMGRFD 7491

RESULT 12
Q748S8 GEOSL
ID Q748S8 GEOSL PRELIMINARY; PRT; 272 AA.
AC Q748S8;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Glutamate racemase (EC 5.1.1.3).
GN Name=mxr1; OrderedLocuNames=GSU2923;
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OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Delaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
OX NCBI_TaxID=35554;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304; DOI=10.1126/science.1088727;
RA Mehe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Beaman M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., Deboy R.T., Durkin A.S.,
RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Weidman J.E., Khouri H.M., Feldblyum T.V., Romero C., Forberger H.A.,
RA Van Aken S.E., Lovley D.R., Fraser C.M.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments.";
RU Science 302:1967-1969 (2003).
DR EMBL; AE017180; AAR36315.1; -; Genomic_DNA.
DR HSSP; P56868; 1B74.
DR TIGR; GSU2923; -.
DR GO; GO:0008881; F:glutamate racemase activity; IEA.
DR GO; GO:0016853; P:isomerase activity; IEA.
DR GO; GO:0009252; P:peptidoglycan biosynthesis; IEA.
DR InterPro; IPR004391; Asp/Glu_rac.
DR InterPro; IPR001920; Asp/Glu_rac.
DR Pfam; PF01177; Asp_Glu_rac; 1.
DR TIGRFAMs; TIGR00067; glut_rac; 1.
DR PROSITE; PS00923; ASP_GLU_RACEMASE_1; 1.
DR PROSITE; PS00924; ASP_GLU_RACEMASE_2; 1.
KW Complete proteome; Isomerase.
SQ SEQUENCE 272 AA; 29521 MW; 674BA01437EC4163 CRC64;

Query Match 63.6%; Score 42; DB 2; Length 272;
Best Local Similarity 60.0%; Pred. No. 80;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PWEVLGYFDS 11
DB 2 PWEVLGYFDS 11

RESULT 13
Q6KIT5 ORYSA PRELIMINARY; PRT; 381 AA.
AC Q6KIT5;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DS Hypothetical protein OSJNBa0038P01.38.
GN Name=OSJNBa0038P01.38;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhachiaceae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=T. Matsumoto T., Katayose Y.;
RT "Oryza sativa nippondare (GAJ) genomic DNA, chromosome 2, BAC
RT clone:OSJNBa0038P01.";
RT Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP06457; BAD22515.1; -; Genomic_DNA.
DR Gramene; Q6KIT5; -.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
KW Hypothetical protein.
SQ SEQUENCE 381 AA; 42714 MW; A50564C2F7224FC4 CRC64;

Query Match 63.6%; Score 42; DB 2; Length 381;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;

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Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVGY 8
DB 176 GPMELVGY 183

RESULT 14
Q8TV9 METAC PRELIMINARY; PRT; 454 AA.
AC Q8TV9;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DS Hypothetical protein MA3668.
GN OrderedlocusNames=MA3668;
OS Methanococcus acetivorans.
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=1193238; DOI=10.1101/gr.223902;
RA Galagan J.E., Nisbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArelano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Telamas J., Turrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf M.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RU Genome Res. 12:532-542(2002).
DR EMBL; AE011076; AAM07023.1; -; Genomic_DNA.
DR InterPro; IPR010180; Cas_CXXC_CXXC.
DR TIGRFAMs; TIGR01908; cas_CXXC_CXXC; 1.
KW Complete proteome.
SQ SEQUENCE 454 AA; 52893 MW; 2BBD6A6E629B0A0 CRC64;

Query Match 63.6%; Score 42; DB 2; Length 454;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVGY 9
DB 319 GPMELVGY 327

RESULT 15
Q8D959 VIBVU PRELIMINARY; PRT; 578 AA.
ID Q8D959_VIBVU
AC Q8D959;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DS Methyl-accepting chemotaxis protein.
GN OrderedlocusNames=VV12747;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=672;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.D., Moon Y.H., Jeong H.,
RA Choy H.B.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
RT Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AE016806; AA011091.1; -; Genomic_DNA.
 DR HSSP; P02942; 1OU7.
 DR GO; GO:0019866; C:inner membrane; IEA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0006935; P:chemotaxis; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR004089; Chmtaxis transd.
 DR InterPro; IPR003660; His_kin_HAMP.
 DR Pfam; PF00672; HAMP; 1.
 DR Pfam; PF00015; MCPsignal; 1.
 DR SMART; SM00304; HAMP; 1.
 DR SMART; SM00283; MA; 1.
 DR PROSITE; PS50111; CHEMOTAXIS_TRANSDUC_2; 1.
 DR PROSITE; PS50885; HAMP; 1.
 KW Complete proteome.
 SQ SEQUENCE 578 AA; 63178 MW; 55004ADCT356DA18 CRC64;

Query Match 63.6%; Score 42; DB 2; Length 578;
 Best Local Similarity 75.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 3 WELVGYFD 10
 |||:||||
 Db 204 WELIGYID 211

Search completed: December 4, 2005, 04:52:22
 Job time : 102.375 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 03:59:51 ; Search time 23.6042 Seconds
(without alignments)
38.528 Million cell updates/sec

Title: US-10-632-706-128

Perfect score: 66

Sequence: 1 GPMELVGYFDS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	62.1	12	1	US-08-264-093-17
2	41	62.1	121	1	US-08-264-093-3
3	39	59.1	274	2	US-09-902-540-14253
4	38	57.6	332	2	US-09-561-763-5
5	38	57.6	332	2	US-09-431-367B-5
6	38	57.6	493	2	US-09-949-016-10836
7	38	57.6	1207	2	US-09-976-594-4
8	37	56.1	427	2	US-09-902-540-15261
9	37	56.1	484	2	US-09-543-681A-6615
10	36	54.5	132	2	US-09-311-021-162
11	36	54.5	140	2	US-09-698-341-29
12	36	54.5	174	2	US-09-902-540-11916
13	36	54.5	194	1	US-08-260-202A-15
14	36	54.5	194	1	US-08-260-202A-24
15	36	54.5	194	1	US-08-017-114-15
16	36	54.5	194	1	US-08-017-114-17
17	36	54.5	194	1	US-08-505-307-15
18	36	54.5	194	2	US-08-505-307-17
19	36	54.5	194	2	US-09-609-151A-15
20	36	54.5	194	2	US-09-609-151A-17
21	36	54.5	194	4	PCT-US94-02034-15
22	36	54.5	194	4	PCT-US94-02034-17
23	36	54.5	206	2	US-09-902-540-16467
24	36	54.5	235	2	US-09-252-991A-29814
25	36	54.5	266	2	US-09-252-991A-21116
26	36	54.5	321	2	US-09-134-000C-3783
27	36	54.5	500	2	US-09-538-092-831

28	36	54.5	521	2	US-09-221-294-2	Sequence 2, Appl1
29	36	54.5	589	2	US-09-489-039A-8395	Sequence 8395, Ap
30	36	54.5	710	2	US-09-518-550-28	Sequence 28, Appl
31	36	54.5	729	2	US-10-104-047-3450	Sequence 3450, Ap
32	36	54.5	751	2	US-09-252-991A-22770	Sequence 22770, A
33	36	54.5	792	2	US-09-994-192-2	Sequence 2, Appl1
34	36	54.5	797	2	US-09-994-192-4	Sequence 4, Appl1
35	36	54.5	1542	2	US-09-949-016-9215	Sequence 9215, Ap
36	36	54.5	3177	1	US-08-477-451-4	Sequence 4, Appl1
37	36	54.5	5532	2	US-09-914-286-6	Sequence 6, Appl1
38	35	53.0	61	2	US-08-978-741-3	Sequence 3, Appl1
39	35	53.0	61	2	US-09-333-729A-5	Sequence 5, Appl1
40	35	53.0	99	2	US-09-390-134B-45	Sequence 45, Appl1
41	35	53.0	142	2	US-09-902-540-13948	Sequence 13948, A
42	35	53.0	160	2	US-09-668-673B-7	Sequence 7, Appl1
43	35	53.0	160	2	US-10-389-532-7	Sequence 7, Appl1
44	35	53.0	166	2	US-09-302-626B-52	Sequence 52, Appl1
45	35	53.0	166	2	US-09-303-518D-886	Sequence 886, App

ALIGNMENTS

RESULT 1
US-08-264-093-17
Sequence 17, Application US/08264093
Parent No. 5639863
GENERAL INFORMATION:
APPLICANT: Michael D. Dan
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESS: Ridout & Maybee
STREET: 2300 Richmond-Adelaide Centre
STREET: 101 Richmond Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 2J7
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 MB storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 6.00
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,093
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA: No. 5639863 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELEPHONE: (416) 868-1482
TELEFAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: not applicable
TOPOLOGY: linear
US-08-264-093-17
Query Match
Best Local Similarity 62.1%; Score 41; DB 1; Length 12;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
DB 1 GPMELVGYFD 10
2 GVMDLNLYFD 11

RESULT 2

US-08-264-093-3

Sequence 3, Application US/08264093

Patent No. 5639863

GENERAL INFORMATION:

APPLICANT: Michael D. Dan

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO

TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE

TITLE OF INVENTION: ANTIGEN

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ridout & Maybee

STREET: 2300 Richmond-Adelaide Centre

CITY: Toronto

STATE: Ontario

COUNTRY: Canada

ZIP: M5H 2J7

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: MS-DOS 6.00

SOFTWARE: ASCII Editor

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/264,093

FILING DATE:

CLASSIFICATION: 536

PRIOR APPLICATION DATA: No. 5639863 applicable

ATTORNEY/AGENT INFORMATION:

NAME: Lake, James R.

REGISTRATION/DOCKET NUMBER: 31081

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 868-1482

TELEFAX: (416) 362-0823

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 121 amino acids

TYPE: amino acid

STRANDEDNESS: not applicable

TOPOLOGY: linear

US-08-264-093-3

Query Match

Best Local Similarity 62.1%; Score 41; DB 1; Length 121;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

DB

1 GPMELVGYFD 10

100 GWMDLNLYFD 109

RESULT 3

US-09-902-540-14253

Sequence 14253, Application US/09902540

Patent No. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 14253

LENGTH: 274

TYPE: PRT

ORGANISM: Myxococcus xanthus

US-09-902-540-14253

Query Match

Best Local Similarity 59.1%; Score 39; DB 2; Length 274;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DB

3 WELVGYFDS 11

153 WNLKGYFDT 161

RESULT 4

US-09-561-763-5

Sequence 5, Application US/09561763

Patent No. 6664373

GENERAL INFORMATION:

APPLICANT: Curtis, Rory A.J. et al.

TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

FILE REFERENCE: MNI-074CP2

CURRENT APPLICATION NUMBER: US/09/561,763

CURRENT FILING DATE: 2000-04-29

PRIOR APPLICATION NUMBER: 09/431,367

PRIOR FILING DATE: 01-11-1999

PRIOR APPLICATION NUMBER: US 09/259,951

PRIOR FILING DATE: 01-03-1999

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 5

LENGTH: 332

TYPE: PRT

ORGANISM: Homo sapiens

US-09-561-763-5

Query Match

Best Local Similarity 57.6%; Score 38; DB 2; Length 332;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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1 GPMELVGYF 9

99 GRMELVGSF 107

RESULT 5

US-09-431-367B-5

Sequence 5, Application US/09431367B

Patent No. 6670149

GENERAL INFORMATION:

APPLICANT: Curtis, Rory A.J.

TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

FILE REFERENCE: MNI-074CP

CURRENT APPLICATION NUMBER: US/09/431,367B

CURRENT FILING DATE: 1999-11-01

PRIOR APPLICATION NUMBER: 09/259,951

PRIOR FILING DATE: 1999-03-01

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 5

LENGTH: 332

TYPE: PRT

ORGANISM: Homo sapiens

US-09-431-367B-5

Query Match

Best Local Similarity 57.6%; Score 38; DB 2; Length 332;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB

1 GPMELVGYF 9

99 GRMELVGSF 107

RESULT 6

US-09-431-367B-5

Sequence 5, Application US/09431367B

Patent No. 6670149

GENERAL INFORMATION:

APPLICANT: Curtis, Rory A.J.

TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR

FILE REFERENCE: MNI-074CP

CURRENT APPLICATION NUMBER: US/09/431,367B

CURRENT FILING DATE: 1999-11-01

PRIOR APPLICATION NUMBER: 09/259,951

PRIOR FILING DATE: 1999-03-01

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 5

LENGTH: 332

TYPE: PRT

ORGANISM: Homo sapiens

US-09-431-367B-5


```
US-09-949-016-10836
; Sequence 10836, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10836
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10836

Query Match          57.6%; Score 38; DB 2; Length 493;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 2 GPMELVGYFDS 11
   |||:|||||
Db 69 PMTKVDYFDN 78

RESULT 7
US-09-976-594-4
; Sequence 4, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 1207
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1863336CD1
US-09-976-594-4

Query Match          57.6%; Score 38; DB 2; Length 1207;
Best Local Similarity 77.8%; Pred. No. 3.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GPMELVGYF 9
   |||:|||||
Db 389 GPTNAVGT 397

RESULT 8
US-09-902-540-15261
; Sequence 15261, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.

US-09-543-681A-6615
; Sequence 6615, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709, 1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6615
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6615

Query Match          56.1%; Score 37; DB 2; Length 484;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 3 WEIVGYFDS 11
   |||:|||||
Db 155 WALIGYQS 163

RESULT 10
US-09-311-021-162
; Sequence 162, Application US/09311021
; Patent No. 6706869
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6300-11A
; CURRENT APPLICATION NUMBER: US/09/311,021
; CURRENT FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 162
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-311-021-162

Query Match 54.5%; Score 36; DB 2; Length 132;
Best Local Similarity 55.6%; Pred. No. 59;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPMELVGYF 9
|||:|
Db 121 GPMDELPRF 129

RESULT 11

US-09-698-341-29
; Sequence 29, Application US/09698341
; Patent No. 6946273
; GENERAL INFORMATION:
; APPLICANT: Sarge, Joseph
; APPLICANT: Hurlbut Hogrefe, Holly
; TITLE OF INVENTION: Compositions and Methods Utilizing DNA Polymerases
; FILE REFERENCE: 25436/1560
; CURRENT APPLICATION NUMBER: US/09/698,341
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: 60/162,600
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Thermococcus sp. JDF-3
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (92)...(92)
; OTHER INFORMATION: X = Unknown
US-09-699-341-29

Query Match 54.5%; Score 36; DB 2; Length 140;
Best Local Similarity 50.0%; Pred. No. 63;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GPMELVGYF 10
|||:|
Db 55 GPMDELPRF 64

RESULT 12
US-09-902-540-13916
; Sequence 13916, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13916
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13916

Query Match 54.5%; Score 36; DB 2; Length 174;
Best Local Similarity 85.7%; Pred. No. 81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LVGYFDS 11

Db 6 LVGYFDS 12
|||:|

RESULT 13
US-08-260-202A-15
; Sequence 15, Application US/08260202A
; Patent No. 5573910
; GENERAL INFORMATION:
; APPLICANT: Deretic, Vojo
; APPLICANT: Martin, Daniel W.
; TITLE OF INVENTION: DETECTION OF CONVERSION TO MUCOID IN
; PSEUDOMONAS AERUGINOSA INFECTING CYSTIC FIBROSIS PATIENTS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/260,202A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,202
; FILING DATE: 15-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/017,114
; FILING DATE: 12-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSK:221\HOD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-260-202A-15

Query Match 54.5%; Score 36; DB 1; Length 194;
Best Local Similarity 71.4%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVGY 7
|||:|
Db 81 GPMRWG 87

RESULT 14
US-08-260-202A-24
; Sequence 24, Application US/08260202A
; Patent No. 5573910
; GENERAL INFORMATION:
; APPLICANT: Deretic, Vojo
; APPLICANT: Martin, Daniel W.
; TITLE OF INVENTION: DETECTION OF CONVERSION TO MUCOID IN
; PSEUDOMONAS AERUGINOSA INFECTING CYSTIC FIBROSIS PATIENTS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433

CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/260,202A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,202
FILING DATE: 15-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/017,114
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hodgins, Daniel S.
REGISTRATION NUMBER: 31,026
REFERENCE/DOCKET NUMBER: UTSK:221/HOD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-260-202A-24

Query Match 54.5%; Score 36; DB 1; Length 194;
Best Local Similarity 71.4%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVG 7
||| :||
Db 81 GPMRMVG 87

RESULT 15
US-08-017-114-15
Sequence 15, Application US/08017114
Patent No. 5591838
GENERAL INFORMATION:
APPLICANT: Detecic, Vojo
APPLICANT: Martin, Daniel W.
TITLE OF INVENTION: DETECTION OF CONVERSION TO MUCOIDY IN
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/017,114
FILING DATE: 19930212
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hodgins, Daniel S.
REGISTRATION NUMBER: 31,026
REFERENCE/DOCKET NUMBER: UTSK:205/HOD

TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/320-7200
TELEFAX: 512/474-7577
TELEX: N/A
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-017-114-15

Query Match 54.5%; Score 36; DB 1; Length 194;
Best Local Similarity 71.4%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVG 7
||| :||
Db 81 GPMRMVG 87

Search completed: December 4, 2005, 04:09:43
Job time : 23.6042 secs

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GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: December 4, 2005, 04:07:28 ; Search time 78.833 Seconds
(without alignments)
58.302 Million cell updates/sec

Title: US-10-632-706-128

Perfect score: 66

Sequence: 1 GPWELVGYFDS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	100.0	11	US-10-632-706-128	Sequence 128, App
2	45	68.2	290	US-10-156-761-9341	Sequence 9341, Ap
3	44	66.7	306	US-10-282-122A-73455	Sequence 73455, A
4	44	66.7	367	US-10-282-122A-74966	Sequence 74966, A
5	44	66.7	367	US-10-282-122A-75801	Sequence 75801, A
6	42	63.6	381	US-10-437-963-192224	Sequence 192224, A
7	41	62.1	125	US-10-425-115-253365	Sequence 253365, A
8	41	62.1	171	US-10-424-599-186545	Sequence 186545, A
9	41	62.1	475	US-10-282-122A-48377	Sequence 48377, A
10	41	62.1	475	US-10-437-963-187947	Sequence 187947, A
11	41	62.1	792	US-10-481-032A-252	Sequence 252, App
12	41	62.1	1352	US-11-097-143-29418	Sequence 29418, A
13	40	60.6	50	US-10-424-599-182764	Sequence 182764, A
14	40	60.6	78	US-10-425-115-319649	Sequence 319649, A
15	40	60.6	146	US-10-477-527-21	Sequence 21, Appl
16	40	60.6	160	US-10-425-115-333207	Sequence 333207, A
17	40	60.6	477	US-10-425-114-70098	Sequence 70098, A
18	40	60.6	507	US-10-424-599-229226	Sequence 229226, A
19	40	60.6	891	US-10-425-115-229314	Sequence 229314, A
20	40	60.6	931	US-10-732-923-22388	Sequence 22388, A
21	40	60.6	949	US-10-732-923-22387	Sequence 22387, A
22	40	60.6	1355	US-10-437-963-110486	Sequence 110486, A
23	39	58.8	511	US-10-425-114-52508	Sequence 52508, A
24	39	58.1	118	US-10-424-599-157468	Sequence 157468, A
25	39	59.1	207	US-10-424-599-153966	Sequence 153966, A
26	39	59.1	235	US-10-732-923-22418	Sequence 22418, A
27	39	59.1	460	US-10-424-599-224678	Sequence 224678, A

28	39	59.1	522	US-10-437-963-194057	Sequence 194057, A
29	39	59.1	537	US-10-739-930-10546	Sequence 10546, A
30	39	59.1	658	US-10-437-963-121136	Sequence 121136, A
31	39	59.1	670	US-10-282-122A-46814	Sequence 46814, A
32	39	59.1	696	US-10-450-763-50763	Sequence 50763, A
33	39	59.1	949	US-10-732-923-22382	Sequence 22382, A
34	39	59.1	949	US-10-732-923-22383	Sequence 22383, A
35	39	59.1	954	US-10-437-963-204079	Sequence 204079, A
36	39	59.1	1199	US-10-437-963-121132	Sequence 121132, A
37	39	59.1	1441	US-10-437-963-111662	Sequence 111662, A
38	38	57.6	48	US-09-764-891-3713	Sequence 3713, Ap
39	38	57.6	71	US-10-425-115-277808	Sequence 277808, A
40	38	57.6	84	US-10-437-963-150254	Sequence 150254, A
41	38	57.6	96	US-10-437-963-141911	Sequence 141911, A
42	38	57.6	135	US-10-424-599-205846	Sequence 205846, A
43	38	57.6	167	US-10-767-701-60011	Sequence 60011, A
44	38	57.6	185	US-10-424-599-230098	Sequence 230098, A
45	38	57.6	207	US-10-425-114-53925	Sequence 53925, A

ALIGNMENTS

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RESULT 1
US-10-632-706-128
; Sequence 128, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSOORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632, 706
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400, 721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144, 806
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 128
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-128

Query Match      100.0%; Score 66; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00072;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 GPWELVGYFDS 11
Db      1 GPWELVGYFDS 11

RESULT 2
US-10-156-761-9341
; Sequence 9341, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: ISHIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156, 761
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; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9341
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9341

Query Match      68.2%; Score 45; DB 4; Length 290;
Best Local Similarity 77.8%; Pred. No. 38;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      3  WELVGFDS 11
      |||:|||||
Db      171 WMLIGYFDS 179

RESULT 3
US-10-282-122A-73455
; Sequence 73455, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73455
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Salomonella paratyphi A
US-10-282-122A-73455

Query Match      66.7%; Score 44; DB 4; Length 306;
Best Local Similarity 69.2%; Pred. No. 58;
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Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy      1  GPWELV---GYF 9
      |||:|||||
Db      66  GPWELVLPFGYF 78

RESULT 4
US-10-282-122A-74966
; Sequence 74966, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74966
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Salomonella typhimurium
US-10-282-122A-74966

Query Match      66.7%; Score 44; DB 4; Length 367;
Best Local Similarity 69.2%; Pred. No. 69;
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy      1  GPWELV---GYF 9
      |||:|||||
Db      127  GPWELVLPFGYF 139

RESULT 5
US-10-282-122A-75801
; Sequence 75801, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
```

APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyckind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282.122A
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 75801
LENGTH: 367
TYPE: PRT
ORGANISM: *Salmonella typhi*
US-10-282-122A-75801

Query Match 66.7%; Score 44; DB 4; Length 367;
Best Local Similarity 69.2%; Pred. No. 69;
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 GPMELV---GYF 9
||| ||| |||
Db 127 GPMELVLCGPGYF 139

RESULT 6
US-10-437-963-192224
Sequence 192224, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 192224
LENGTH: 381

TYPE: PRT
ORGANISM: *Oryza sativa*
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_88472C.1.pep
US-10-437-963-192224

Query Match 63.6%; Score 42; DB 4; Length 381;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVGF 8
||| ||| |||
Db 176 GPMELTGF 183

RESULT 7
US-10-425-115-253365
Sequence 253365, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 253365
LENGTH: 125
TYPE: PRT
ORGANISM: *Zea mays*
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_16264C.1.pep
US-10-425-115-253365

Query Match 62.1%; Score 41; DB 4; Length 125;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVGF 9
||| ||| |||
Db 75 GPMELKGF 83

RESULT 8
US-10-424-599-186545
Sequence 186545, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 186545
LENGTH: 171
TYPE: PRT
ORGANISM: *Glycine max*
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_139463C.1.pep
US-10-424-599-186545

Query Match 62.1%; Score 41; DB 4; Length 171;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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OY 1 GPMELVGYFD 10
|||: |||
Db 14 GPMDEMKYFD 23

RESULT 9
US-10-282-122A-48377
; Sequence 48377, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-09-06
; PRIOR FILING DATE: 2000-09-06
; PRIOR FILING DATE: 2000-09-09
; PRIOR FILING DATE: 2000-09-09
; PRIOR FILING DATE: 2000-10-23
; PRIOR FILING DATE: 2000-10-23
; PRIOR FILING DATE: 2000-11-27
; PRIOR FILING DATE: 2000-11-27
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-16
; Remaining prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48377
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Bacteroides fragilis
US-10-282-122A-48377

Query Match 62.1%; Score 41; DB 4; Length 475;
Best Local Similarity 54.5%; Pred. No. 2.7e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 GPMELVGYFD 11
|||: |||
Db 404 GPMKLIYYDS 414

RESULT 10
US-10-437-963-187947
; Sequence 187947, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbasuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 187947
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(475)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_845C.1.pep
US-10-437-963-187947

Query Match 62.1%; Score 41; DB 4; Length 475;
Best Local Similarity 70.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GPMELVGYFD 10
|||: |||
Db 115 GPMESGKYHD 124

RESULT 11
US-10-481-032A-252
; Sequence 252, Application US/10481032A
; Publication No. US20050177901A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Cheng, Wenqiong
; APPLICANT: Briggs, Steven
; APPLICANT: Cooper, Bret
; APPLICANT: Goff, Stephen A.
; APPLICANT: Moughamer, Todd
; APPLICANT: Glazebrook, Jane
; APPLICANT: Katagiri, Fumitaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicolas
; APPLICANT: Rike, Darrell
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 60148USPCT
; CURRENT FILING DATE: 2003-12-16
; PRIOR FILING DATE: 2003-12-16
; PRIOR FILING DATE: 2001-06-22
; PRIOR FILING DATE: 2001-06-22
; PRIOR FILING DATE: 2001-09-26
; PRIOR FILING DATE: 2001-09-26
; PRIOR FILING DATE: 2001-12-20
; PRIOR FILING DATE: 2001-12-20
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 1201
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 252
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(14)
; OTHER INFORMATION: Xaa = any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)..(16)
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OTHER INFORMATION: Xaa = any naturally occurring amino acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (399)..(399)
OTHER INFORMATION: Xaa = any naturally occurring amino acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (493)..(493)
OTHER INFORMATION: Xaa = any naturally occurring amino acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (669)..(669)
OTHER INFORMATION: Xaa = any naturally occurring amino acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (671)..(671)
OTHER INFORMATION: Xaa = any naturally occurring amino acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (673)..(673)
OTHER INFORMATION: Xaa = any naturally occurring amino acid
US-10-481-032A-252

Query Match 62.1%; Score 41; DB 5; Length 792;
Best Local Similarity 66.7%; Pred. No. 4.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PWEVLGYD 10
Db 245 PWEVLGYD 253

RESULT 12
US-11-097-143-29418
Sequence 29418, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
FILE REFERENCE: CL000728
CURRENT FILING DATE: 2005-04-04
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: Pse-Seq for Windows Version 4.0
SEQ ID NO 29418
LENGTH: 1352
TYPE: PRT
ORGANISM: DROSOPHILA
US-11-097-143-29418

Query Match 62.1%; Score 41; DB 6; Length 1352;
Best Local Similarity 77.8%; Pred. No. 7.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WEVLGYFDS 11
Db 161 WRNVLGYFDS 169

RESULT 13
US-10-424-599-182764
Sequence 182764, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovallik David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 182764
LENGTH: 50
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_13604C.1.pep
US-10-424-599-182764

Query Match 60.6%; Score 40; DB 4; Length 50;
Best Local Similarity 66.7%; Pred. No. 48;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPWEVLGYF 9
Db 32 GKWEVLGYF 40

RESULT 14
US-10-425-115-319649
Sequence 319649, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovallik, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 319649
LENGTH: 78
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_54590C.1.pep
US-10-425-115-319649

Query Match 60.6%; Score 40; DB 4; Length 78;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPWEVLGYF 9
Db 21 GPWEVLGYF 29

RESULT 15
US-10-477-527-21
Sequence 21, Application US/10477527
Publication No. US20040171807A1

GENERAL INFORMATION:
; APPLICANT: The Trustees of the University of Pennsylvania
; APPLICANT: Gao, Guangping
; APPLICANT: Wilson, James M.
; TITLE OF INVENTION: Method for Rapid Screening of Bacterial Transformants and Novel S
; TITLE OF INVENTION: Adenovirus Proteins
; FILE REFERENCE: UPV-N2630PCT
; CURRENT APPLICATION NUMBER: US/10/477,527
; PRIOR FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/300,501
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/385,632
; PRIOR FILING DATE: 2002-06-04
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 146
; TYPE: PRT
; ORGANISM: chimpanzee C68 adenovirus protein
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (62)..(62)
; OTHER INFORMATION: Xaa can be any amino acid
US-10-477-527-21

Query Match 60.6%; Score 40; DB 4; Length 146;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPMELVG 7
|||:|
Db 101 GPMELVG 107

Search completed: December 4, 2005, 04:37:29
Job time : 79.833 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:08:08 ; Search time 3.20833 Seconds
(without alignments)
16.417 Million cell updates/sec

Title: US-10-632-706-128
Perfect score: 66
Sequence: 1 GPMELVGFDS 11

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:

- 1: /cgn2_6/ptodata/1/pubpaa/US09_NEM_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEM_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEM_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US08_NEM_PUB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/PCT_NEM_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US10_NEM_PUB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEM_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEM_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	54.5	792	6	US-10-467-657-6026
2	36	54.5	792	6	US-10-467-657-7528
3	35	53.0	356	6	US-10-467-657-1210
4	34	51.5	322	7	US-11-074-176-36
5	34	51.5	723	6	US-10-467-657-1916
6	34	51.5	926	6	US-10-841-129-2
7	33.5	50.8	478	7	US-11-037-829A-4
8	33	50.0	198	7	US-11-082-389-302
9	33	50.0	281	7	US-11-082-389-304
10	33	50.0	431	7	US-11-082-389-304
11	33	50.0	724	6	US-10-131-826A-60
12	33	50.0	1510	7	US-11-055-822-72
13	33	50.0	2725	7	US-11-113-424-52
14	32	48.5	456	6	US-10-467-657-4150
15	32	48.5	533	6	US-10-467-657-4150
16	32	48.5	771	7	US-11-147-047-33
17	31.5	47.7	532	7	US-11-184-380-6
18	31.5	47.7	544	6	US-10-719-311-18
19	31.5	47.7	588	6	US-11-184-380-5
20	31.5	47.7	598	6	US-10-719-311-16
21	31.5	47.7	724	7	US-11-184-380-4
22	31.5	47.7	734	6	US-10-719-311-4
23	31.5	47.7	735	6	US-11-184-380-24
24	31	47.0	142	6	US-10-821-234-1030
25	31	47.0	229	6	US-10-510-366-228

26	31	47.0	290	6	US-10-793-626-214	Sequence 214, App
27	31	47.0	393	6	US-10-821-234-1292	Sequence 1292, App
28	31	47.0	490	6	US-10-131-826A-310	Sequence 310, App
29	31	47.0	626	6	US-10-467-657-6426	Sequence 6426, App
30	31	47.0	626	6	US-10-467-657-7618	Sequence 7618, App
31	31	47.0	745	7	US-11-109-156-14	Sequence 14, App
32	31	47.0	766	6	US-10-522-789-2	Sequence 2, App
33	30	45.5	31	6	US-10-467-657-2188	Sequence 2188, App
34	30	45.5	180	6	US-10-665-455-11	Sequence 11, App
35	30	45.5	221	7	US-11-055-822-82	Sequence 82, App
36	30	45.5	389	6	US-10-979-821-2	Sequence 2, App
37	30	45.5	400	6	US-10-793-626-3116	Sequence 3116, App
38	30	45.5	450	6	US-10-467-657-2126	Sequence 2126, App
39	30	45.5	457	7	US-11-055-822-80	Sequence 80, App
40	30	45.5	479	6	US-10-821-234-871	Sequence 871, App
41	30	45.5	934	7	US-10-858-730-8	Sequence 8, App
42	30	45.5	1857	7	US-11-102-217-2	Sequence 2, App
43	29.5	44.7	178	6	US-10-939-890-116	Sequence 116, App
44	29.5	44.7	178	6	US-10-508-263-32	Sequence 32, App
45	29.5	44.7	178	6	US-10-508-263-46	Sequence 46, App

ALIGNMENTS

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RESULT 1
US-10-467-657-6026
Sequence 6026, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: Seqwin99, version 1.04
SEQ ID NO 6026
LENGTH: 792
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6026

Query Match      54.5%: Score 36; DB 6; Length 792;
Best Local Similarity 75.0%: Pred. No. 27;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      4 ELVGFDS 11
      ||:||||:
Db      390 ELVGFDS 397

RESULT 2
US-10-467-657-7528
Sequence 7528, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8

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;; PRIOR FILING DATE: 2001-02-12
;; NUMBER OF SEQ ID NOS: 9218
;; SOFTWARE: SeqMn9, version 1.04
;; SEQ ID NO 7528
;; LENGTH: 792
;; TYPE: PRT
;; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7528

Query Match 54.5%; Score 36; DB 6; Length 792;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 ELVGYFDS 11
||:||||:
Db 390 ELVGYFDN 397

RESULT 3
US-10-467-657-1210
;; Sequence 1210, Application US/10467657
;; Publication No. US20050260581A1
;; GENERAL INFORMATION:
;; APPLICANT: CHIRON SPA
;; APPLICANT: FONTANA Maria Rita
;; APPLICANT: PIZZA Mariagrazia
;; APPLICANT: MASIGNANI Vega
;; APPLICANT: MONACI Elisabetta
;; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
;; FILE REFERENCE:
;; CURRENT APPLICATION NUMBER: US/10/467,657
;; CURRENT FILING DATE: 2003-08-11
;; PRIOR APPLICATION NUMBER: GB-0103424.8
;; PRIOR FILING DATE: 2001-02-12
;; NUMBER OF SEQ ID NOS: 9218
;; SOFTWARE: SeqMn9, version 1.04
;; SEQ ID NO 1210
;; LENGTH: 356
;; TYPE: PRT
;; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1210

Query Match 53.0%; Score 35; DB 6; Length 356;
Best Local Similarity 62.5%; Pred. No. 19;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVGY 8
||:||||:
Db 45 GIMENLGY 52

RESULT 4
US-11-074-176-36
;; Sequence 36, Application US/11074176
;; Publication No. US20050250135A1
;; GENERAL INFORMATION:
;; APPLICANT: Kleenhammer, Todd R.
;; APPLICANT: Russell, William M.
;; APPLICANT: Allemann, Eric
;; APPLICANT: McAniff, Olivia
;; APPLICANT: Perilli, Andrea Azcarate
;; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
;; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
;; FILE REFERENCE: 5051-694
;; CURRENT APPLICATION NUMBER: US/11/074,176
;; CURRENT FILING DATE: 2005-03-07
;; PRIOR APPLICATION NUMBER: 60/551,161
;; PRIOR FILING DATE: 2004-03-08
;; NUMBER OF SEQ ID NOS: 381
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 36
;; LENGTH: 322
;; TYPE: PRT

;; ORGANISM: Lactobacillus acidophilus
US-11-074-176-36

Query Match 51.5%; Score 34; DB 7; Length 322;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ELVGYFD 10
||:||||:
Db 43 ELVGYFD 49

RESULT 5
US-10-467-657-1916
;; Sequence 1916, Application US/10467657
;; Publication No. US20050260581A1
;; GENERAL INFORMATION:
;; APPLICANT: CHIRON SPA
;; APPLICANT: FONTANA Maria Rita
;; APPLICANT: PIZZA Mariagrazia
;; APPLICANT: MASIGNANI Vega
;; APPLICANT: MONACI Elisabetta
;; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
;; FILE REFERENCE:
;; CURRENT APPLICATION NUMBER: US/10/467,657
;; CURRENT FILING DATE: 2003-08-11
;; PRIOR APPLICATION NUMBER: GB-0103424.8
;; PRIOR FILING DATE: 2001-02-12
;; NUMBER OF SEQ ID NOS: 9218
;; SOFTWARE: SeqMn9, version 1.04
;; SEQ ID NO 1916
;; LENGTH: 723
;; TYPE: PRT
;; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1916

Query Match 51.5%; Score 34; DB 6; Length 723;
Best Local Similarity 53.3%; Pred. No. 55;
Matches 8; Conservative 0; Mismatches 1; Indels 6; Gaps 1;

QY 1 GPMELV-----GYF 9
||:||||:
Db 260 GPMELVNSAAGYF 274

RESULT 6
US-10-841-129-2
;; Sequence 2, Application US/10841129
;; Publication No. US20050250113A1
;; GENERAL INFORMATION:
;; APPLICANT: Zuker, Charles S.
;; APPLICANT: Erlenbach, Isolda
;; APPLICANT: Hoon, Mark A.
;; APPLICANT: Ryba, Nicholas J. P.
;; APPLICANT: Zhang, Yifeng
;; APPLICANT: The Regents of the University of California
;; APPLICANT: The Government of the United States of America
;; APPLICANT: as represented by The Secretary of the
;; APPLICANT: Department of Health and Human Services
;; TITLE OF INVENTION: A Mammalian Magnesium/Manganese Sensing G Protein
;; TITLE OF INVENTION: Coupled Receptor
;; FILE REFERENCE: 02307E-145400US
;; CURRENT APPLICATION NUMBER: US/10/841,129
;; CURRENT FILING DATE: 2004-05-07
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 2
;; LENGTH: 926
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: human magnesium/manganese sensing G protein
;; OTHER INFORMATION: coupled receptor (GPCR) R5.24, Mg receptor, Mn

```
; OTHER INFORMATION: receptor
US-10-841-129-2
Query Match      51.5%; Score 34; DB 6; Length 926;
Best Local Similarity 83.3%; Pred. No. 70;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy      2 PWELVG 7
        |||||
Db      443 PWELIG 448

RESULT 7
US-11-037-829A-4
; Sequence 4, Application US/11037829A
; Publication No. US20050255551A1
; GENERAL INFORMATION:
; APPLICANT: Targacept, Inc
; APPLICANT: Catholic Healthcare West
; APPLICANT: Benchrif, Merouane
; APPLICANT: Lukas, Ronald J.
; TITLE OF INVENTION: Methods and Compositions Relating to Chimeric
; FILE REFERENCE: T103 1520.PCT
; CURRENT APPLICATION NUMBER: US/11/037,829A
; PRIOR FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US 60/397,380
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-037-829A-4

Query Match      50.8%; Score 33.5; DB 7; Length 478;
Best Local Similarity 58.3%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

Oy      1 GPWELVG---YF 9
        |||||
Db      207 GWEELGLVLPYF 218

RESULT 8
US-11-082-389-302
; Sequence 302, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Krogger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; PRIOR FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-06-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
```

```
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 302
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 4
; OTHER INFORMATION: Xaa = Phe, Ser, Tyr, or Cys
US-11-082-389-302

Query Match      50.0%; Score 33; DB 7; Length 198;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy      3 WELVGY 8
        |||||
Db      99 WQLIGY 104

RESULT 9
US-11-082-389-304
; Sequence 304, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Krogger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; PRIOR FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 304
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-304
```

Query Match 50.0%; Score 33; DB 7; Length 281;
 Best Local Similarity 66.7%; Pred. No. 33;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 3 WEIVGY 8
 Db 153 WOLIGY 158

RESULT 10
 US-11-055-822-76
 ; Sequence 76, Application US/11055822
 ; Publication No. US20050260707A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pompeius, Markus
 ; APPLICANT: Kroeger, Burkhard
 ; APPLICANT: Schoder, Hartwig
 ; APPLICANT: Zeider, Oskar
 ; APPLICANT: Haberhauser, Gregor
 ; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
 ; FILE REFERENCE: BGI-121PCN
 ; CURRENT APPLICATION NUMBER: US/11/055,822
 ; PRIOR FILING DATE: 2005-02-11
 ; PRIOR APPLICATION NUMBER: 09/606,740
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: 60/141,031
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: 60/142,101
 ; PRIOR FILING DATE: 1999-07-02
 ; PRIOR APPLICATION NUMBER: 60/148,613
 ; PRIOR FILING DATE: 1999-08-12
 ; PRIOR APPLICATION NUMBER: 60/187,970
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: DE 19930476.9
 ; PRIOR FILING DATE: 1999-07-01
 ; PRIOR APPLICATION NUMBER: DE 19931415.2
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931418.7
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931419.5
 ; PRIOR FILING DATE: 1999-07-08
 ; PRIOR APPLICATION NUMBER: DE 19931420.9
 ; PRIOR FILING DATE: 1999-07-08
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 1158
 ; SEQ ID NO 76
 ; LENGTH: 431
 ; TYPE: PRT
 ; ORGANISM: Corynebacterium glutamicum
 US-11-055-822-76

Query Match 50.0%; Score 33; DB 7; Length 431;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPWEL 5
 Db 284 GPWEL 288

RESULT 11
 US-10-131-826A-60
 ; Sequence 60, Application US/10131826A
 ; Publication No. US20050245730A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerltsen, Mary E.

APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P330R1C128
 ; CURRENT APPLICATION NUMBER: US/10/131,826A
 ; PRIOR FILING DATE: 2002-04-24
 ; PRIOR APPLICATION NUMBER: 60/049911
 ; PRIOR FILING DATE: 1997-06-18
 ; PRIOR APPLICATION NUMBER: 60/056974
 ; PRIOR FILING DATE: 1997-08-26
 ; PRIOR APPLICATION NUMBER: 60/059113
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059115
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059117
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059122
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059184
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059352
 ; PRIOR FILING DATE: 1997-09-19
 ; PRIOR APPLICATION NUMBER: 60/059588
 ; PRIOR FILING DATE: 1997-09-19
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 60
 ; LENGTH: 724
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-131-826A-60

Query Match 50.0%; Score 33; DB 6; Length 724;
 Best Local Similarity 50.0%; Pred. No. 82;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 WEIVGYFD 10
 Db 83 WDIVGYFD 90

RESULT 12
 US-11-055-822-72
 ; Sequence 72, Application US/11055822
 ; Publication No. US20050260707A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pompeius, Markus
 ; APPLICANT: Kroeger, Burkhard
 ; APPLICANT: Schoder, Hartwig
 ; APPLICANT: Zeider, Oskar
 ; APPLICANT: Haberhauser, Gregor
 ; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
 ; FILE REFERENCE: BGI-121PCN
 ; CURRENT APPLICATION NUMBER: US/11/055,822
 ; PRIOR FILING DATE: 2005-02-11
 ; PRIOR APPLICATION NUMBER: 09/606,740
 ; PRIOR FILING DATE: 2000-06-23
 ; PRIOR APPLICATION NUMBER: 60/141,031
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: 60/142,101
 ; PRIOR FILING DATE: 1999-07-02

```

; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See file Wrapper or PLM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 72
; LENGTH: 1510
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-72
```

```
Query Match          50.0%; Score 33; DB 7; Length 1510;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GPWEL 5
      |||||
Db      1063 GPWEL 1067
```

```

RESULT 13
US-11-113-424-52
; Sequence 52, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; PRIOR FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 2725
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-424-52
```

```
Query Match          50.0%; Score 33; DB 7; Length 2725;
Best Local Similarity 60.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 GPWELVGYFD 10
      |||||
```

```
Db      503 GPWYLAIFYND 512
```

```

RESULT 14
US-10-467-657-4150
; Sequence 4150, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTRANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 4150
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4150
```

```
Query Match          48.5%; Score 32; DB 6; Length 456;
Best Local Similarity 57.1%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 PWEIATY 8
      |||||
Db      154 PWEIATY 160
```

```

RESULT 15
US-11-147-047-33
; Sequence 33, Application US/11147047
; Publication No. US2005026068A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankej
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, ZhaoYing
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GPS0016
; CURRENT APPLICATION NUMBER: US/11/147,047
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221,097
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-147-047-33
```

```
Query Match          48.5%; Score 32; DB 7; Length 533;
Best Local Similarity 83.3%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Oy	2	PWELVG	7
Db	178	PWEAVG	183

Search completed: December 4, 2005, 04:37:49
Job time : 4.20833 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:09:54 ; Search time 130.312 Seconds
(without alignments)
50.576 Million cell updates/sec

Title: US-10-632-706-197
Perfect score: 89
Sequence: 1 EPDMLMGDRGALDV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_21:*

1: geneeqp1980s:*

2: geneeqp1990s:*

3: geneeqp2000s:*

4: geneeqp2001s:*

5: geneeqp2002s:*

6: geneeqp2003as:*

7: geneeqp2003bs:*

8: geneeqp2004s:*

9: geneeqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	89	100.0	15	ADR38727	Adt38727 Mouse hea
2	89	100.0	15	ADR38728	Adt38728 Mouse hea
3	89	100.0	15	ADR38792	Adt38792 Mouse hea
4	89	100.0	15	ADR38795	Adt38795 Mouse hea
5	89	100.0	15	ADR38798	Adt38798 Mouse hea
6	89	100.0	15	ADR38729	Adt38729 Mouse hea
7	89	100.0	15	ADR38801	Adt38801 Mouse hea
8	51	57.3	334	ABG20331	Abg20331 Novel hum
9	48	53.9	201	ADJ98189	Adj98189 Prochlo
10	48	53.9	229	ABO66015	AbO66015 Klebsiell
11	48	53.9	775	AAI13560	Aai13560 Streptomy
12	47	52.8	59	AAI48365	Aai48365 Human pro
13	47	52.8	455	ABG22524	Abg22524 Novel hum
14	47	52.8	904	ADS23387	AdS23387 Bacterial
15	46	51.7	186	AAW24399	Aaw24399 Human EST
16	45	50.6	54	ABP03542	Abp03542 Human ORF
17	45	50.6	372	ABU04048	Abu04048 Protein e
18	45	50.6	450	ADN47961	Adn47961 Thermococ
19	45	50.6	614	ADP06781	Adp06781 Bacterial
20	44	49.4	70	AAI15847	Aai15847 Arabidops
21	44	49.4	137	ADA21119	Ada21119 Human sec
22	44	49.4	342	AAAB1737	AaB1737 Human sec
23	44	49.4	409	AAAB6393	AaB6393 Putative
24	44	49.4	472	ADC68881	Adc68881 Human GPC

25	44	49.4	687	8	ADS42446	AdS42446 Bacterial
26	43	48.3	100	8	ADP065091	Adp065091 Novel hum
27	43	48.3	345	2	AAI38595	Aai38595 Neisseria
28	43	48.3	345	2	ABE49036	AbE49036 N. gonorr
29	43	48.3	383	3	AAI38596	Aai38596 Neisseria
30	43	48.3	383	6	ABP79536	Abp79536 N. gonorr
31	43	48.3	383	3	ABE49038	AbE49038 N. gonorr
32	43	48.3	546	2	AAW26164	Aaw26164 KF-1 prot
33	43	48.3	582	4	AAU30396	Aau30396 Novel hum
34	43	48.3	616	8	ADS20416	AdS20416 Crab-eat
35	43	48.3	683	2	AAW26163	Aaw26163 Mouse KF-
36	43	48.3	683	9	ADZ04210	AdZ04210 Novel apo
37	43	48.3	685	2	AAW26165	Aaw26165 Human KF-
38	43	48.3	685	9	ADZ07646	AdZ07646 Cyclin-de
39	43	48.3	685	9	ADZ04207	AdZ04207 Novel apo
40	43	48.3	732	9	ABM94428	Abm94428 M. xanthu
41	43	48.3	2519	7	ABM88218	Abm88218 Rice abio
42	42.5	47.8	315	4	ABB09181	Abb09181 Pseudomon
43	42.5	47.8	315	6	ABU15664	Abu15664 Protein e
44	42.5	47.8	320	7	ABO69555	AbO69555 Pseudomon
45	42	47.2	53	4	AAU65794	Aau65794 Propionib

ALIGNMENTS

RESULT 1
ID ADR38727 standard; peptide, 15 AA.
AC ADR38727;
DT 02-DEC-2004 (first entry)
DE Mouse heavy chain variable region CDR3 seqid 129.
XX anti-bacterial; antibody; botulinum neurotoxin type A; BoNT/A;
XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
XX toxin neutralisation; botulinum neurotoxin poisoning; mouse;
XX heavy chain variable region; complementarily determining region; CDR3.
OS Mus sp.
XX
XX US2004175385-A1.
XX
XX 09-SEP-2004.
XX
XX 01-AUG-2003; 2003US-00632706.
XX
XX 31-AUG-1998; 98US-00144886.
XX 01-AUG-2002; 2002US-0400721P.
XX (REGC) UNIV CALIFORNIA.
XX Marks JD, Amerdorter P;
XX WPI; 2004-652009/63.
XX
XX New isolated antibody that neutralizes botulinum neurotoxin type A,
XX useful for diagnosing botulism or for treating pathologies associated
XX with botulinum neurotoxin poisoning.
XX
XX Example 3; SEQ ID NO 129; 110pp; English.
XX
XX The invention describes an isolated antibody (I) that specifically binds
XX to an epitope specifically bound by an antibody expressed by a specific
XX clone where (I) binds to and neutralises botulinum neurotoxin type A
XX (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
XX specifically bound by an antibody expressed by a clone chosen from clone
XX S25, C35, C39, I66, 3D12, B4, I63, nuc25, A11, A12, WRI(V), WRI(T), 3-1,
XX 3-8, 3-10 and IN61, where (I) binds to and neutralizes botulinum
XX neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
XX comprising BoNT/A neutralising epitope having an epitope that is

CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC ; producing (I) ; and a composition (II) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I) ; and a kit comprising (I). (I) is useful for neutralising
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain variable region complementarity determining
CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.
CC
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 89; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EPDWLWMDRGALDV 15
Db 1 EPDWLWMDRGALDV 15
RESULT 2
ADR38728 standard; peptide; 15 AA.
XX
XX ADR38728;
XX
XX 02-DEC-2004 (first entry)
XX
XX Mouse heavy chain variable region CDR3 seqid 130.
XX
XX
XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
XX toxin neutralisation; botulinum neurotoxin poisoning; mouse;
XX heavy chain variable region; complementarity determining region; CDR3.
XX
XX Mus sp.
XX
XX US2004175385-A1.
XX
XX PN 09-SEP-2004.
XX
XX PF 01-AUG-2003; 2003US-00632706.
XX
XX PR 31-AUG-1998; 98US-00144886.
XX
XX PR 01-AUG-2002; 2002US-0400721P.
XX
XX PA (REGC) UNIV CALIFORNIA.
XX
XX PI Marks JD, Amerdorfer P;
XX
XX PI MPI; 2004-652009/63.
XX
XX DR New isolated antibody that neutralizes botulinum neurotoxin type A,
XX PT useful for diagnosing botulism or for treating pathologies associated
XX PT with botulinum neurotoxin poisoning.
XX
XX PS Example 3; SEQ ID NO 130; 110pp; English.
XX
XX The invention describes an isolated antibody (I) that specifically binds
XX to an epitope specifically bound by an antibody expressed by a specific
XX clone where (I) binds to and neutralises botulinum neurotoxin type A
XX (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
XX specifically bound by an antibody expressed by a clone chosen from clone
XX S25, C25, C39, IC6, JD12, B4, 1F3, huc25, Ar1, Ar2, WRI(V), WRI(T), 3-1,

CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
CC comprising BoNT/A neutralising epitope having an epitope that is
CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC ; producing (I) ; and a composition (III) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I) ; and a kit comprising (I). (I) is useful for neutralising
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain variable region complementarity determining
CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.
CC
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 89; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EPDWLWMDRGALDV 15
Db 1 EPDWLWMDRGALDV 15
RESULT 3
ADR38792 standard; peptide; 15 AA.
XX
XX ADR38792;
XX
XX 02-DEC-2004 (first entry)
XX
XX Mouse heavy chain anti-BoNT-antibody CD3 seqid 194.
XX
XX
XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
XX toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
XX CDR3; complementarity determining region 1.
XX
XX Mus sp.
XX
XX OS US2004175385-A1.
XX
XX PN 09-SEP-2004.
XX
XX PD 01-AUG-2003; 2003US-00632706.
XX
XX PR 31-AUG-1998; 98US-00144886.
XX
XX PR 01-AUG-2002; 2002US-0400721P.
XX
XX PA (REGC) UNIV CALIFORNIA.
XX
XX PI Marks JD, Amerdorfer P;
XX
XX PI MPI; 2004-652009/63.
XX
XX DR New isolated antibody that neutralizes botulinum neurotoxin type A,
XX PT useful for diagnosing botulism or for treating pathologies associated
XX PT with botulinum neurotoxin poisoning.
XX
XX PS Example 4; SEQ ID NO 194; 110pp; English.
XX
XX The invention describes an isolated antibody (I) that specifically binds
XX to an epitope specifically bound by an antibody expressed by a specific
XX clone where (I) binds to and neutralises botulinum neurotoxin type A

(BONT/A). An isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a clone chosen from clone S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1, 3-8, 3-10 and INM1, where (I) binds to and neutralizes botulinum neurotoxin type A (BONT/A). Also described are: a polypeptide (II) comprising BONT/A neutralising epitope having an epitope that is specifically bound by an antibody expressed by clones as mentioned in (I); producing (I); and a composition (III) comprising several anti-botulinum neurotoxin antibodies, where each antibody is specific for a different epitope of a botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. The following are disclosed: a pharmaceutical composition comprising (I); and a kit comprising (I). (I) is useful for neutralising BONT/A antibody and for neutralising a botulinum neurotoxin which involves contacting neurotoxin with (I) in surplus, where each of (I) is specific for a different epitope of the botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. (I) is useful for diagnosing the botulinum or for treating pathologies associated with botulinum neurotoxin poisoning. (I) exhibits specificity and affinity towards BONT/A. (I) enables rapid detection or diagnosis of botulism. This is the amino acid sequence of mouse heavy chain anti-BONT-antibody CDR3.

XX Sequence 15 AA;

SQ Query Match 100.0%; Score 89; DB 8; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.8e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPDMLMGDRGALDV 15

1 EPDMLMGDRGALDV 15

Db 1 EPDMLMGDRGALDV 15

RESULT 4
ADR38795
ID ADR38795 standard; peptide; 15 AA.

XX ADR38795;

XX 02-DEC-2004 (first entry)

XX Mouse heavy chain anti-BONT-antibody CDR3 seqid 197.

XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
XX BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
XX toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
XX CDR3; complementarity determining region 1.

XX Mus sp.

XX US2004175385-A1.

XX 09-SEP-2004.

XX 01-AUG-2003; 2003US-00632706.

XX 31-AUG-1998; 98US-00144886.

XX 01-AUG-2002; 2002US-0400721P.

XX (REGC) UNIV CALIFORNIA.

XX Marks JD, Amerdorfer P;

XX WPI; 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,
XX PT useful for diagnosing botulism or for treating pathologies associated
XX PT with botulinum neurotoxin poisoning.

XX Example 4; SEQ ID NO 197; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds

CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralises botulinum neurotoxin type A
CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
CC 3-8, 3-10 and INM1, where (I) binds to and neutralizes botulinum
CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
CC comprising BONT/A neutralising epitope having an epitope that is
CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC; producing (I); and a composition (III) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC BONT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain anti-BONT-antibody CDR3.

XX Sequence 15 AA;

SQ Query Match 100.0%; Score 89; DB 8; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.8e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPDMLMGDRGALDV 15

1 EPDMLMGDRGALDV 15

Db 1 EPDMLMGDRGALDV 15

RESULT 5
ADR38798
ID ADR38798 standard; peptide; 15 AA.

XX ADR38798;

XX 02-DEC-2004 (first entry)

XX Mouse heavy chain anti-BONT-antibody CDR3 seqid 200.

XX antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
XX BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
XX toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
XX CDR3; complementarity determining region 1.

XX Mus sp.

XX US2004175385-A1.

XX 09-SEP-2004.

XX 01-AUG-2003; 2003US-00632706.

XX 31-AUG-1998; 98US-00144886.

XX 01-AUG-2002; 2002US-0400721P.

XX (REGC) UNIV CALIFORNIA.

XX Marks JD, Amerdorfer P;

XX WPI; 2004-652009/63.
XX New isolated antibody that neutralizes botulinum neurotoxin type A,
XX PT useful for diagnosing botulism or for treating pathologies associated
XX PT with botulinum neurotoxin poisoning.

XX Example 4; SEQ ID NO 200; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralizes botulinum neurotoxin type A
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
 CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
 CC comprising BoNT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I) and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I) and a kit comprising (I). (I) is useful for neutralising
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulinum
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain anti-BoNT-antibody CDR3.

CC Sequence 15 AA;

CC Query Match 100.0%; Score 89; DB 8; Length 15;

CC Best Local Similarity 100.0%; Pred. No. 1.8e-06;

CC Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPDWLWMDRGALDV 15
 |||||
 Db 1 EPDWLWMDRGALDV 15

RESULT 6
 ADR38729
 ID ADR38729 standard; peptide; 15 AA.

AC ADR38729;

DT 02-DEC-2004 (first entry)

DE Mouse heavy chain variable region CDR3 seqid 131.

XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
 XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 XX toxin neutralisation; botulinum neurotoxin poisoning; mouse;
 XX heavy chain variable region; complementarity determining region; CDR3.

OS Mus sp.

PN US2004175385-A1.

PD 09-SEP-2004.

PF 01-AUG-2003; 2003US-00632706.

PR 31-AUG-1998; 98US-00144886.

PR 01-AUG-2002; 2002US-0400721P.

XX (REGC) UNIV CALIFORNIA.

PI Marks JD, Amersdorfer P;

XX WPI; 2004-652009/63.

PT New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.

XX Example 3; SEQ ID NO 131, 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
 CC 3-8, 3-10 and ING1, where (I) binds to and neutralises botulinum
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
 CC comprising BoNT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I) and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I) and a kit comprising (I). (I) is useful for neutralising
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulinum
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain variable region complementarity determining
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.

CC Sequence 15 AA;

CC Query Match 100.0%; Score 89; DB 8; Length 15;

CC Best Local Similarity 100.0%; Pred. No. 1.8e-06;

CC Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPDWLWMDRGALDV 15
 |||||
 Db 1 EPDWLWMDRGALDV 15

RESULT 7
 ADR38801
 ID ADR38801 standard; peptide; 15 AA.

AC ADR38801;

DT 02-DEC-2004 (first entry)

DE Mouse heavy chain anti-BoNT-antibody CDR3 seqid 203.

XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
 XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
 XX toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
 XX CDR3; complementarity determining region 1.

OS Mus sp.

PN US2004175385-A1.

PD 09-SEP-2004.

PF 01-AUG-2003; 2003US-00632706.

PR 31-AUG-1998; 98US-00144886.

PR 01-AUG-2002; 2002US-0400721P.

XX (REGC) UNIV CALIFORNIA.

PI Marks JD, Amersdorfer P;

XX WPI; 2004-652009/63.

PT New isolated antibody that neutralizes botulinum neurotoxin type A,
PT useful for diagnosing botulism or for treating pathologies associated
PT with botulinum neurotoxin poisoning.
XX

PS Example 4; SEQ ID NO 203; 110pp; English.
XX

CC The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralises botulinum neurotoxin type A
CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
CC 3-8, 3-10 and IN01, where (I) binds to and neutralises botulinum
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
CC comprising BoNT/A neutralising epitope having an epitope that is
CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC ; producing (I); and a composition (III) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain anti-BoNT-antibody CDR3.
XX

SQ Sequence 15 AA;
XX

Query Match 84.3%; Score 75; DB 8; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00023;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 EPPDLWGDRGALDV 15
||| ||||| |||||
Db 1 EPPDLWGDRGALDV 15

RESULT 8

ABG20331
ID ABG20331 standard; protein; 334 AA.

XX ABG20331;
AC

DT 13-FEB-2002 (first entry)
XX

DE Novel human diagnostic protein #20322.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX

OS Homo sapiens.
XX

FN WO200175067-A2.
XX

PD 11-OCT-2001.
XX

PF 30-MAR-2001; 2001WO-US008631.
XX

PR 31-MAR-2000; 2000US-00540217.
XX

PR 23-AUG-2000; 2000US-00649167.
XX

PA (HYSE-) HYSEQ INC.
XX

PI Drmanac RT, Liu C, Tang YT;
XX

DR WPI; 2001-639362/73.
DR N-PSDB; AAS84518.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensic, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX

PS Claim 20; SEQ ID NO 50690; 103pp; English.
XX

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensic, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 334 AA;
XX

Query Match 57.3%; Score 51; DB 4; Length 334;
Best Local Similarity 53.3%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 1 EPPDLWGDRGALDV 15
: ||| ||| : |||
Db 263 KPMSSWGPSPGWIDV 277

RESULT 9

ADJ98189
ID ADJ98189 standard; protein; 201 AA.

XX ADJ98189;
AC

DT 06-MAY-2004 (first entry)
XX

DE Prochlorococcus marinus str MIT 9313 phyto kinase protein.

XX phyto kinase; tocopherol biosynthesis; plant; drought resistance;
KW enzyme.
XX

OS Prochlorococcus marinus str. MIT 9313.
XX

FN WO2004013312-A2.
XX

PD 12-FEB-2004.
XX

PF 05-AUG-2003; 2003WO-US025276.
XX

PR 05-AUG-2002; 2002US-0400689P.
XX

PR 05-AUG-2003; 2003US-00634548.
XX

PA (MONS) MONSANTO TECHNOLOGY LLC.
XX

PI Norris SR, Lincoln K, Abad MS, Bilers R, Hartsuyker KK;
XX

PI Hirschberg J, Karunanandaa B, Moshiri F, Stein JC, Valentin HB;
XX

DR WPI; 2004-157125/15.
DR

PT New phyto1 kinase polynucleotides, useful in mediating tocopherol
 PT biosynthesis and in producing plants with increased drought resistance.
 PS Claim 1; SEQ ID NO 27; 189pp; English.
 XX
 CC The invention relates to a novel substantially purified nucleic acid
 CC molecule encoding a phyto1 kinase. The nucleic acid molecules and
 CC polypeptides of the invention may be useful in mediating tocopherol
 CC biosynthesis and in producing plants with increased drought resistance.
 CC The current sequence is that of a phyto1 kinase protein of the invention.
 XX
 SQ Sequence 201 AA;
 QY
 Query Match 53.9%; Score 48; DB 8; Length 201;
 Best Local Similarity 50.0%; Pred. No. 39;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 Db 2 PDMILMGDRGAL 13
 123 PNMILMGQRKSI 134

RESULT 10
 ABO66015
 ID ABO66015 standard; protein; 229 AA.
 XX
 AC ABO66015;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Klebsiella pneumoniae polypeptide seqid 12532.
 XX
 KM Recombinant expression vector; transcription regulatory element;
 KM Klebsiella pneumoniae protein; antibacterial; Vaccine.
 OS Klebsiella pneumoniae.
 XX
 PN US6610836-B1.
 XX
 PD 26-AUG-2003.
 XX
 PF 27-JAN-2000; 2000US-00489039.
 XX
 PR 29-JAN-1999; 99US-0117747P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Breton GL, Osborne M;
 XX
 DR WPI; 2003-895346/82.
 DR N-PSDB; ACH99566.
 PT
 PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
 PT preparing a vaccine composition against Klebsiella pneumoniae.
 PS Disclosure; SEQ ID NO 12532; 932pp; English.
 XX
 CC The invention describes a new isolated nucleic acid encoding a Klebsiella
 CC pneumoniae polypeptide. Also described are: a recombinant expression
 CC vector comprising the nucleic acid, operably linked to a transcription
 CC regulatory element; and a cell comprising the recombinant expression
 CC vector. The nucleic acid is useful for preparing a vaccine composition
 CC against Klebsiella pneumoniae. This is the amino acid sequence of a
 CC Klebsiella pneumoniae polypeptide of the invention
 XX
 SQ Sequence 229 AA;

Query Match 53.9%; Score 48; DB 7; Length 229;
 Best Local Similarity 57.1%; Pred. No. 44;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EPDMLMGDRGALD 14
 | | | | | | | |

Db 32 ERSWCKMGDRPAID 45
 RESULT 11
 ID AAB13560 standard; protein; 775 AA.
 XX
 AC AAB13560;
 XX
 DT 06-MAR-2001 (first entry)
 XX
 DE Streptomyces globisporus C-1027 gene cluster ORF -1.
 XX
 KM Eneidyne C-1027 biosynthesis gene cluster; apoprotein; chromophore;
 KM open reading frame -1; cancer.
 XX
 OS Streptomyces globisporus.
 XX
 PN WO200040596-A1.
 XX
 PD 13-JUL-2000.
 XX
 PF 06-JAN-2000; 2000WO-US000446.
 XX
 PR 06-JAN-1999; 99US-0115434P.
 XX
 PR 05-JAN-2000; 2000US-00477962.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Shen B, Liu W, Christenson SD, Strandage S;
 XX
 DR WPI; 2000-465947/40.
 DR N-PSDB; AAA63348; AAA63349.
 XX
 PT Isolated nucleic acid comprising a nucleic acid encoding any of C-1027
 PT open reading frames (ORFs) -7 to 42, excluding ORF 9 (cagA), useful for
 PT the production of enediyne C-1027 antitumor antibiotics.
 XX
 PS Claim 15; Page 87-91; 160pp; English.
 XX
 CC The present sequence is the protein which is encoded by open reading
 CC frame -1 of the Streptomyces globisporus enediyne C-1027 gene cluster.
 CC Eneidyne C-1027 is an antibiotic, consisting of an apoprotein and a non-
 CC peptidic chromophore, which acts by damaging DNA. The sequences within
 CC the gene cluster, and the proteins they encode, can be used in the
 CC treatment of cancer, along with antagonists of the protein. This protein
 CC is an ABC transport/UvrA-like protein
 XX
 SQ Sequence 775 AA;

Query Match 53.9%; Score 48; DB 3; Length 775;
 Best Local Similarity 53.8%; Pred. No. 1.6e+02;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 2 PDMILMGDRGALD 14
 | | | | | | | |
 Db 195 PDWOIWAQSGRLD 207

RESULT 12
 ID AAY48365 standard; protein; 59 AA.
 XX
 AC AAY48365;
 XX
 DT 08-DEC-1999 (first entry)
 XX
 DE Human prostate cancer-associated protein 62.
 XX
 KM Expressed sequence tag; EST; prostate; tumor; treatment; gene therapy;
 KM cancer; tissue specificity; human.
 XX
 OS Homo sapiens.

XX DE19811194-A1.
PN 16-SEP-1999.
XX
XX
XX 10-MAR-1998; 98DE-01011194.
XX
XX 10-MAR-1998; 98DE-01011194.
XX
XX (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
XX Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
PI WPI: 1999-519629/44.
XX
XX N-PSDB: AAZ33505.
XX
XX New nucleic acid expressed at high level in normal prostatic tissue and
PT encoded polypeptides, used to treat cancer and screen for therapeutic
XX agents.
XX
XX Claim 22: 148; 194pp; German.
XX
XX This invention describes novel nucleic acid sequences (A) that are
CC expressed at high level in normal prostatic tissue. Polypeptides (I)
CC encoded by (A) are used; (a) for identifying agents for treatment of
CC prostatic cancer and (b) for therapy of prostate cancer, optionally where
CC expressed by gene therapy methods. (A) is also used to isolate full-
CC length genes (for gene therapy) and for recombinant production of (I),
CC which can be used to raise specific antibodies. (A) are identified by
CC assembly of ESTs (expressed sequence tags) before these are analyzed for
CC expression pattern (tissue specificity). This approach eliminates many of
CC the false results, as regards tissue specificity, associated with known
CC methods that use single (usually short) ESTs. AA18304-148456 represent
CC peptides encoded by the expressed sequence tags described in the method
CC of the invention
XX
XX Sequence 59 AA;
SQ
Query Match 52.8%; Score 47; DB 2; Length 59;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 WLLMGDRG 11
| | | | |
Db 44 WLLMGSRG 51
RESULT 13
ABG22524
ID ABG22524 standard; protein; 455 AA.
XX
XX ABG22524;
AC
XX
XX 18-FEB-2002 (first entry)
DT
XX
XX Novel human diagnostic protein #22515.
DE
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
OS
XX
XX WO200175067-A2.
PN
XX
XX 11-OCT-2001.
PD
XX
XX 30-MAR-2001; 2001WO-US008631.
PF
XX
XX 31-MAR-2000; 2000US-00540217.
PR
XX
XX 23-AUG-2000; 2000US-00649167.
XX
XX (HYSB-) HYSBQ INC.
XX

PI Drmanac RT, Liu C, Tang YT;
XX
XX WPI: 2001-639362/73.
XX
XX N-PSDB: AAS86711.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 20: SEQ ID NO 52883; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridization probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG0377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 455 AA;
SQ
Query Match 52.8%; Score 47; DB 4; Length 455;
Best Local Similarity 53.8%; Pred. No. 1,3e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EPDWLWGRGAL 13
| : | | | : | | :
Db 93 EQNWLWRCRGVM 105
RESULT 14
ADS23387
ID ADS23387 standard; protein; 904 AA.
XX
XX ADS23387;
AC
XX
XX 02-DEC-2004 (first entry)
DT
XX
XX Bacterial polypeptide #12420.
DE
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmotic;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
XX Bacteria.
OS
XX
XX US2003233675-A1.
PN
XX
XX 18-DEC-2003.
PD
XX
XX 20-FEB-2003; 2003US-00369493.
PF
XX
XX 21-FEB-2002; 2002US-0360039P.
PR
XX
XX

PA (CHAO/) CHAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX
 DR WPI; 2004-061375/06.
 XX
 PT New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX
 PS Claim 1; SEQ ID NO 12420; 122pp; English.
 XX
 CC The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 CC
 XX
 SQ Sequence 904 AA;
 Query Match 52.8%; Score 47; DB 8; Length 904;
 Best Local Similarity 70.0%; Pred. No. 2.6e+02;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 4 WILMGDRGAL 13
 Db 460 WILMGDKTSL 469
 RESULT 15
 AAM24399
 ID AAM24399 standard; protein; 186 AA.
 XX
 AC AAM24399;
 XX
 DT 12-OCT-2001 (first entry)
 XX
 DE Human EST encoded protein SEQ ID NO: 1924.
 XX
 KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
 KW gene therapy; nutrition.
 XX
 OS Homo sapiens.
 XX
 PN WO200154477-A2.
 XX
 PD 02-AUG-2001.
 XX

PF 25-JAN-2001; 2001WO-US002687.
 XX
 PR 25-JAN-2000; 2000US-00491404.
 PR 17-JUL-2000; 2000US-00617746.
 PR 03-AUG-2000; 2000US-00631451.
 PR 15-SEP-2000; 2000US-00663870.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Aundi V,
 PI Cao Y, Dermanac RA, Zhang J, Werhman T;
 XX
 DR WPI; 2001-476164/51.
 DR N-PSDB; AAH99058.
 XX
 PT Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use.
 XX
 PS Claim 20; Page 1235; 1275pp; English.
 XX
 CC The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a
 CC protein of the invention
 XX
 SQ Sequence 186 AA;
 Query Match 51.7%; Score 46; DB 4; Length 186;
 Best Local Similarity 53.3%; Pred. No. 71;
 Matches 8; Conservative 3; Mismatches 2; Indels 2; Gaps 1;
 QY 2 PDWILMG--DRGALD 14
 Db 168 PGWILMGKRNKRGILN 182
 Search completed: December 4, 2005, 04:44:59
 Job time : 132.312 secs

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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:45 ; Search time 21.25 Seconds
(without alignments)
67.918 Million cell updates/sec

Title: US-10-632-706-197

Sequence: 1 EPDMLMGDRGALDV 15

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	51.7	373	2 D71142	hypothetical prote
2	45.5	51.1	298	2 AE3234	transcriptional re
3	45	50.6	203	2 G70595	probable endo prot
4	45	50.6	601	2 AG0066	probable AMP-bind
5	44.5	50.0	1076	2 T30842	serine-repeat anti
6	44	49.4	237	2 G82768	virulence protein
7	44	49.4	409	2 B75010	hypothetical prote
8	44	49.4	491	2 T10930	3C3.21 protein - S
9	44	49.4	601	2 B95296	probable ABC-type
10	43	48.3	321	2 S77614	phosphoribosylform
11	43	48.3	462	2 T50432	homolog to yeast o
12	43	48.3	683	2 UC5383	zinc finger protei
13	43	48.3	685	2 UC5392	zinc finger protei
14	43	48.3	698	2 AE2593	hypothetical prote
15	43	47.8	315	2 H83276	probable lipase PA
16	42.5	47.8	139	2 G98356	hypothetical prote
17	42	47.2	139	2 AG2925	hypothetical prote
18	42	47.2	397	2 B53240	allergen Amb a II
19	42	47.2	408	1 A69819	probable phospho
20	42	47.2	482	2 A10554	thiamin biosynthes
21	42	47.2	482	2 B90688	probable oxidoredu
22	42	47.2	482	2 T46944	thiamin biosynthes
23	42	47.2	482	2 A85539	probable oxidoredu
24	42	47.2	482	2 G64771	yeak protein - Esc
25	42	47.2	486	2 T51431	glucosyltransferas
26	42	47.2	486	2 H87311	hypothetical prote
27	42	47.2	492	2 T38156	citrate lyase - fi
28	42	47.2	566	2 H84037	long-chain fatty-a
29	42	47.2	604	2 T49577	hypothetical prote

30	42	47.2	608	2 T34994	probable long-chain
31	42	47.2	804	2 AG0565	probable membrane
32	42	47.2	804	2 G64780	probable membrane
33	42	47.2	804	2 A85549	probable oxidoredu
34	42	47.2	804	2 G90698	probable oxidoredu
35	42	47.2	993	2 B97212	conserved membrane
36	41	46.1	36	2 B84416	hypothetical prote
37	41	46.1	248	2 T36093	probable DNA methy
38	41	46.1	262	2 F75093	hypothetical prote
39	41	46.1	288	2 AG0888	probable Arac-fem
40	41	46.1	359	2 C70735	probable Idsa prot
41	41	46.1	403	2 T10847	yeak protein - Rhi
42	41	46.1	408	2 AG0305	probable L-ldicol
43	41	46.1	438	2 T37786	probable RNA-bind
44	41	46.1	442	2 D84600	probable xylose
45	41	46.1	459	2 T27657	hypothetical prote

ALIGNMENTS

RESULT 1
D71142
hypothetical protein PH0351 - *Pyrococcus horikoshii*
C:Species: *Pyrococcus horikoshii*
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
C:Accession: D71142
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hata, Y.; Hino, Y.; Yamamoto, S.; Sekine, M.; Ohtoku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kishida, N.; Oguchi, DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: D71142
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-373 <KAW>
A:Cross-references: UNIPROT:O58089; UNIPARC:UPI0000062DB7; GB:AF000002; NID:g3236129; PIR
A:Experimental source: strain OT3
A>Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH0351

Query Match 51.7%; Score 46; DB 2; Length 373;
Best Local Similarity 43.5%; Pred. No. 19;
Matches 10; Conservative 1; Mismatches 2; Indels 10; Gaps 1;
Db 2 PDWLLM-----GDRGALD 14
318 PGWLLMGILLLMGRIGNPGALD 340

RESULT 2
AE3234
transcriptional regulator, *lysR* family gcva [imported] - *Agrobacterium tumefaciens* (etra
C:Species: *Agrobacterium tumefaciens*
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AE3234
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AE3234
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-298 <KUR>
A:Cross-references: UNIPROT:Q8U680; UNIPARC:UPI0000002D764; GB:AE008690; PIDN:AAI46291.1;
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: gcva

A:Genome: plasmid
C:Superfamily: regulatory protein ampr

Query Match 51.1%; Score 45.5; DB 2; Length 298;
Best Local Similarity 56.2%; Pred. No. 18;
Matches 9; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy 1 EPDWLW-GDRGALDV 15
Db 199 EPDWLWCAQAGVADV 214

RESULT 3

G70595
probable end protein - Mycobacterium tuberculosis (strain H37Rv)

C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C:Accession: G70595
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sultson, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; PMID:98295987; PMID:9634230

A:Accession: G70595
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-203 <COL>
A:Cross-references: UNIPROT:O05852; UNIPARC:UPI000016534B; GB:Z95120; GB:AL123456; NID:G
A:Experimental source: strain H37Rv

C:Genetics:
A:Gene: entc
C:Superfamily: cofactor-dependent phosphoglycerate mutase; phosphoglycerate mutase homol

Query Match 50.6%; Score 45; DB 2; Length 203;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPDWLW 7
Db 103 EPDWLW 109

RESULT 4

AG0066
probable AMP-binding enzyme-family protein YPO0537 [imported] - Yersinia pestis (strain

C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C:Accession: AG0066
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AG0066
A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-601 <KUR>
A:Cross-references: UNIPROT:Q821G5; UNIPARC:UPI000000CD42; GB:AL590842; PIDN:CA089394.1;
C:Genetics:
A:Gene: YPO0537

C:Superfamily: synchocystis long-chain-fatty-acid-CoA ligase; acetate-CoA ligase homol

Query Match 50.6%; Score 45; DB 2; Length 601;
Best Local Similarity 64.3%; Pred. No. 42;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EPDWLW-GDRGALDV 14
Db 440 EDGWLKTGAGALDV 453

RESULT 5
T30842
serine-repeat antigen 3 - Plasmodium vivax

C:Species: Plasmodium vivax
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C:Accession: T30842
R:Kiefer, M.C.; Crawford, K.A.; Boley, L.J.; Landsberg, K.E.; Gibson, H.L.; Kestow, D.C.; Mol. Biochem. Parasitol. 78, 55-65, 1996
A:Title: Identification and cloning of a locus of serine repeat antigen (serra)-related ge

A:Reference number: Z20898; MUID:96408670; PMID:8813677

A:Accession: T30842

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1076 <RIB>
A:Cross-references: UNIPROT:Q26154; UNIPARC:UPI00000809B3; EMBL:U51723; NID:G1381087; PII

C:Genetics:
A:Insertions: 12/1; 253/1; 302/1
A:Note: V-SERA 3
C:Superfamily: Plasmodium vivax serine-repeat antigen

Query Match 50.0%; Score 44.5; DB 2; Length 1076;
Best Local Similarity 40.9%; Pred. No. 87;
Matches 9; Conservative 2; Mismatches 4; Indels 7; Gaps 1;

Qy 1 EPDWLW-----WGDRGALDV 15
Db 743 KPWLWLSWGWKHWGDKTFKCV 764

RESULT 6

G82768
virulence protein XPO754 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C:Accession: G82768
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: G82768
A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-237 <SIM>
A:Cross-references: UNIPROT:Q9PFC4; UNIPARC:UPI00000C24F4; GB:AB003916; GB:AB003849; NID

A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvaranga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrer, H

as-Neto, E.; Docena, C.; El-Dorty, H.; Facinca, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Jungueira, M.L.; Kemp, B.L.; Kleijma, J.P.; Krieger, J.E.; Kuramae, E.B.; Laigr

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, S

A:Authors: Martins, B.M.F.; Matsumura, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmiti, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.J. de M.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvair

M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XFO754
C:Superfamily: type IV secretory pathway, VirC component

Query Match 49.4%; Score 44; DB 2; Length 237;
Best Local Similarity 58.3%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 WLWMDRGALDV 15
Db 151 WLWMDRGALDV 162

RESULT 7
B75010
hypothetical protein PAB1063 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: B75010
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: B75010
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-409 <KAM>
A:Cross-references: UNIPROT:Q9UT92; UNIPARC:UPI0000034560; GB:AJ248288; GB:AL096836; NIT
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB1063

Query Match 49.4%; Score 44; DB 2; Length 409;
Best Local Similarity 39.1%; Pred. No. 41;
Matches 9; Conservative 2; Mismatches 2; Indels 10; Gaps 1;

QY 2 PDWLMW-----GDRGALD 14
Db 354 PGWILMGLILLMGRVGNPGALD 376

RESULT 8
T10930
3C3.21 protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10930
R:Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1998
A:Reference number: Z17215
A:Accession: T10930
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-491 <PAR>
A:Cross-references: UNIPROT:O86654; UNIPARC:UPI00000DAD67; EMBL:AL031231; NID:e1315070;
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: 3C3.21

Query Match 49.4%; Score 44; DB 2; Length 491;
Best Local Similarity 61.5%; Pred. No. 49;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 DWLMGDRGALD 15
Db 413 EFVLHGDRGALD 425

RESULT 9
E95296
probable ABC-type iron transport system protein Sma0525 [imported] - Sinorhizobium meli
C:Species: Sinorhizobium meli
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: E95296
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe
; Kaiman, S.; Keating, D.H.; Palm, C.; Peck, W.C.; Surzycki, R.; Wells, D.H.; Yen, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: E95296
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-601 <KUN>
A:Cross-references: UNIPROT:Q930C1; UNIPARC:UPI00000CB03E; GB:AE006469; PIDN:AAK64935.1;
A:Experimental source: strain 1021, megaplasmid pSymA

R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davies, R.W.; Drenno, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kaiman, S.; Keating, D.H.; Kise, E.; Komp, C.; Lelaure,
hebulc, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yen, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meli
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Sma0525
A:Genome: plasmid

Query Match 49.4%; Score 44; DB 2; Length 601;
Best Local Similarity 85.7%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PDWLMWG 8
Db 169 PDWLMWG 175

RESULT 10
S77614
phosphoribosylformylglycinamide synthase (EC 6.3.5.3) component II - Synecococcus sp.
N:Alternate names: FGAM synthetase
C:Species: Synecococcus sp.
A:Variety: PCC 7942
C:Date: 29-Jul-1997 #sequence_revision 24-Oct-1998 #text_change 31-Dec-2004
C:Accession: S77614; S77613
R:Liu, Y.; Tsinoresmas, N.F.
submitted to the EMBL Data Library, August 1995
A:Description: Unusual gene arrangement for the putative chromosome replication origin a
A:Reference number: S77614
A:Accession: S77614
A:Molecule type: DNA
A:Residues: 1-112 <LIW>
A:Cross-references: UNIPROT:Q55037; UNIPARC:UPI0000176276; EMBL:U33322; NID:g974613; PIDN
A:Experimental source: PCC 7942
R:Liu, Y.; Tsinoresmas, N.F.; Golden, S.S.; Kondo, T.; Johnson, C.H.
Mol. Microbiol. 20, 1071-1081, 1996
A:Title: Circadian expression of genes involved in the purine biosynthetic pathway of cyr
A:Reference number: S77612; MUID:96405630; PMID:8809759
A:Accession: S77613
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 113-321 <LIW>
A:Cross-references: UNIPARC:UPI00000BE4A4; EMBL:U33211
A:Experimental source: PCC 7942
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
C:Genetics:
A:Gene: purL
C:Function:
A:Description: catalyzes the condensation of 5'-phosphoribosylformylglycinamide with ATP,
A:Pathway: purine nucleotide biosynthesis
A:Note: fourth step in pathway
C:Keywords: ligase; purine nucleotide biosynthesis

Query Match 48.3%; Score 43; DB 2; Length 321;
Best Local Similarity 63.6%; Pred. No. 46;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PDWLMGDRGA 12
Db 240 PDWLMFABEGA 250

RESULT 11
T50422
homolog to yeast orf yor166c. [imported] - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C:Accession: T50422

R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, February 2000
A:Reference number: Z25039
A:Accession: J50422
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-462 <SER>
A:Cross-references: UNIPROT:Q9P7J1, UNIPARC:UPI000060AA1B, EMBL:AL157991, PIDN:CA876224.
A:Experimental source: strain 972h(-); cosmid C24B10
C:Genetics:
A:Gene: SPDB:SPCC24B10.15
A:Map position: 3

Query Match 48.3%; Score 43; DB 2; Length 462;
Best Local Similarity 55.6%; Pred. No. 65;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 DMLMGDRG 11
Db 394 EMDLWARG 402

RESULT 12

JC5392
zinc finger protein KF-1 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 04-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
A:Accession: JC5393
R;Yaoojima, K.; Tsujimura, A.; Mizuno, T.; Shigeyoshi, Y.; Inazawa, J.; Kikuno, R.; Kuma

Biochem. Biophys. Res. Commun. 231, 481-487, 1997
A:Title: Cloning of human and mouse cDNAs encoding novel zinc finger proteins expressed

A:Reference number: JC5392; PMID:97223484; PMID:9070305

A:Accession: JC5393

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-683 <YAS>

A:Cross-references: UNIPROT:O08883; UNIPARC:UPI00000E0601; DBJ:D76445; NID:G2058262; PT

A:Experimental source: brain

C:Comment: This protein is involved in membranous protein-sorting apparatus similarly to

C:Genetics:

A:Gene: Kf-1

C:Superfamily: zinc finger protein KF-1 precursor; RING finger homology

C:Keywords: glycoprotein; phosphoprotein; zinc

F:1-19/Domain: signal sequence #status predicted <SIG>

F:326-344/Domain: transmembrane #status predicted <TM1>

F:352-380/Domain: transmembrane #status predicted <TM2>

F:615-666/Domain: RING finger homology <RING>

F:100,155,228,273,301,398,536/Binding site: carbohydrate (Asn) (covalent) #status predic

F:664/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 48.3%; Score 43; DB 2; Length 683;
Best Local Similarity 85.7%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EPDWLW 7
Db 603 EPDWLW 609

RESULT 13

JC5392
zinc finger protein KF-1 precursor - human

C:Species: Homo sapiens (man)

C:Date: 04-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004

C:Accession: JC5392

R;Yaoojima, K.; Tsujimura, A.; Mizuno, T.; Shigeyoshi, Y.; Inazawa, J.; Kikuno, R.; Kuma

Biochem. Biophys. Res. Commun. 231, 481-487, 1997

A:Title: Cloning of human and mouse cDNAs encoding novel zinc finger proteins expressed

A:Reference number: JC5392; PMID:97223484; PMID:9070305

C:Accession: JC5392

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: 1-685 <YAS>
A:Cross-references: UNIPROT:O00237, UNIPARC:UPI000073F2A, DBJ:D76444, NID:G1945614, PIT

A:Experimental source: brain

C:Comment: This protein is involved in membranous protein-sorting apparatus similarly to

C:Genetics:

A:Gene: Kf-1

C:Superfamily: zinc finger protein KF-1 precursor; RING finger homology

C:Keywords: zinc

F:1-19/Domain: signal sequence #status predicted <SIG>

F:326-344/Domain: transmembrane #status predicted <TM1>

F:352-380/Domain: transmembrane #status predicted <TM2>

F:617-668/Domain: RING finger homology <RING>

Query Match 48.3%; Score 43; DB 2; Length 685;
Best Local Similarity 85.7%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EPDWLW 7
Db 605 EPDWLW 611

RESULT 14

A82593
hypothetical protein XF2169 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

A:Accession: A82593

R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; PMID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: A82593

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-698 <STM>

A:Cross-references: UNIPROT:Q9PBH5, UNIPARC:UPI0000C2968; GB:AE004030; GB:AB003849; NID

A:Experimental source: strain 9a5c

R;Simmons, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvaranga, R.; A

Brites, M.R.S.; Bueno, M.R.P.; Canarro, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H

as-Neto, E.; Docena, C.; El-Dorri, H.; Faciniani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitejima, J.P.; Kitzinger, J.E.; Kuramae, E.E.; Laig

Chado, M.A.; Medeira, A.M.B.N.; Medeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, B

A:Authors: Martins, B.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmarini, D.A

Rodrigues, V.; Rosa, A.U. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tsunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF2169

Query Match 48.3%; Score 43; DB 2; Length 698;
Best Local Similarity 63.6%; Pred. No. 97;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 DMLMGDRGAL 13
Db 554 DMLMGDRSL 564

RESULT 15

H83276
probable lipase PA2949 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 12-Jul-2004

C:Accession: H83276

R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br

adman, S.; Yuan Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
A|Reference number: AB2950; MUID:20437337; PMID:10584043
A|Accession: H83276
A|Status: preliminary
A|Molecule type: DNA
A|Residues: 1-315 <STO>
A|Cross-references: UNIPROT:Q9KJG6; UNIPARC:UPI000000C4EC6; GB:AE004721; GB:AE004091, NIT
A|Experimental source: strain PA01
C|Genetics:
A|Gene: PA2949
C|Superfamily: tropinesterase

Query Match	47.8%	Score 42.5;	DB 2;	length 315;
Best Local Similarity	66.7%	Pred. No. 54;		
Matches 10; Conservative	0;	Mismatches 4;	Indels 1;	Gaps 1;

Qy	2	PDWLLWGDRG-ALDV	15
Db	249	PTLLWGDRDRVLDV	263

Search completed: December 4, 2005, 04:53:46
Job time : 33.25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:36 ; Search time 136.875 Seconds
(without alignments)
77.318 Million cell updates/sec

Title: US-10-632-706-197
Perfect score: 89
Sequence: 1 EPDMLWMDRGALDV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50.6	441	2	OSLQ90_SILPO	OSLQ90 silicibacte
2	49.9	208	2	OSYQ86_NOCFA	OSYQ86 nocardia fa
3	49.9	405	2	OSN403_SYNP6	OSN403 synecococc
4	49.9	779	2	Q6H084_FREDI	Q6H084 fredmyella d
5	48.8	217	2	Q7V3U3_PROMM	Q7V3U3 prochlorococ
6	48.8	262	2	Q8BJF9_SHEON	Q8BJF9 shewanella
7	48.8	426	2	Q5SS50_CRYNE	Q5SS50 crytococcu
8	48.8	448	2	Q9S4Z3_SALEN	Q9S4Z3 salmoneilla
9	48.8	775	2	Q9S8A1_CANAL	Q9S8A1 candida alb
10	48.8	784	2	Q8GMI3_STRGL	Q8GMI3 streptomyce
11	48.8	793	2	Q59S70_CANAL	Q59S70 candida alb
12	48.8	804	2	Q8R990_SALTY	Q8R990 salmoneilla
13	47.5	527	2	Q6CDD2_ORYSA	Q6CDD2 oryza sativ
14	47.5	61	2	Q6THZ8_HUMAN	Q6THZ8 homo sapien
15	47.5	364	2	Q7UG34_RHOBA	Q7UG34 rhodospirell
16	47.5	369	2	Q5KNM7_CRYNE	Q5KNM7 crytococcu
17	47.5	375	2	Q55ZB2_CRYNE	Q55ZB2 crytococcu
18	47.5	471	2	Q4RPV5_9SPHN	Q4RPV5 erythrobact
19	47.5	1517	2	Q5AYP9_EMENT	Q5AYP9 aspergillus
20	47.5	1547	2	Q9CLAO_ASPFU	Q9CLAO aspergillus
21	47.5	1547	2	Q4WDD4_ASPFU	Q4WDD4 aspergillus
22	46.6	214	2	Q4UX96_CORJK	Q4UX96 corynebacte
23	46.6	350	1	COBT_PSEBM	Q85W6 pseudomonas
24	46.6	356	2	Q6C182_YARLI	Q6C182 yarrowia li
25	46.6	373	2	Q58089_PYRHO	Q58089 pyrococcus
26	46.6	396	2	Q70GME_CHIRE	Q70GME chlamydomon
27	46.6	1562	2	Q9Y840_MYCRG	Q9Y840 mycoplasmae
28	45.5	266	2	Q7D2M8_AGRTS	Q7D2M8 agrobacteri
29	45.5	298	2	Q8U680_AGRTS	Q8U680 agrobacteri
30	45.5	91	2	Q854E3_9CAUD	Q854E3 mycobacteri
31	45.5	141	2	Q9NU66_HUMAN	Q9NU66 homo sapien

32	45	50.6	203	2	Q6MW27_MYCTU	Q6MW27 mycobacteri
33	45	50.6	203	2	Q7TW28_MYCBO	Q7TW28 mycobacteri
34	45	50.6	228	2	Q7DSX2_MYCBO	Q7DSX2 mycobacteri
35	45	50.6	246	2	Q7U9Y4_SYNPX	Q7U9Y4 synecococc
36	45	50.6	370	2	Q88JL2_PSEBK	Q88JL2 pseudomonas
37	45	50.6	381	2	Q5P2Z9_AZOSB	Q5P2Z9 azoarcus sp
38	45	50.6	450	2	Q5JDB4_PYROK	Q5JDB4 pyrococcus
39	45	50.6	505	2	Q5LR06_SILPO	Q5LR06 silicibacte
40	45	50.6	601	2	Q6ELP9_YERP6	Q6ELP9 yersinia ps
41	45	50.6	601	2	Q8ZIG5_YERP6	Q8ZIG5 yersinia ps
42	45	50.6	781	2	Q4HY20_GIBZE	Q4HY20 gibberella
43	45	50.6	892	2	Q4KIV4_PSEBS	Q4KIV4 pseudomonas
44	45	50.6	907	2	Q4ZN69_PSEBS	Q4ZN69 pseudomonas
45	45	50.6	1326	2	Q6ATH6_ORYSA	Q6ATH6 oryza sativ

ALIGNMENTS

RESULT 1						
ID	OSLQ90_SILPO	PRELIMINARY;	PRT;	441	AA.	
AC	OSLQ90;					
DT	01-FEB-2005 (TREMBlrel. 29, Created)					
DT	01-FEB-2005 (TREMBlrel. 29, Last sequence update)					
DT	01-FEB-2005 (TREMBlrel. 29, Last annotation update)					
DE	TRAP dicarboxylate transporter, DctM subunit.					
GN	OrderedLocustNames=SP02605;					
OC	Silicibacter pomeroyi.					
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;					
OC	Rhodobacteraceae; Silicibacter.					
OX	NCBI_TaxID=89184;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].					
RC	STRAIN=DSB-3 / ATCC 700808 / DSM 15171;					
RX	PubMed=15602564; DOI=10.1038/nature03170;					
RA	Moran M.A., Buchan A., Gonzalez J.M., Heidelberg J.F., Whitman W.B.,					
RA	Kiene R.P., Henriksen J.R., King G.M., Belas R., Fuqua C.,					
RA	Brinkac L.M., Lewis M., Johri S., Weaver B., Pai G., Eisen J.A.,					
RA	Rane E., Sheldon W.M., Ye W., Miller T.R., Carlton J., Raeko D.A.,					
RA	Paulsen I.T., Ren Q., Daugherty S.C., DeBoy R.T., Dodson R.J.,					
RA	Durkin A.S., Madupu R., Nelson W.C., Sullivan S.A., Rosovitz M.J.,					
RA	Haft D.H., Selengut J., Ward N.;					
RT	"Genome sequence of Silicibacter pomeroyi reveals adaptations to the					
RT	marine environment."					
RL	Nature 432:910-913(2004).					
DR	EMBL; CP000031; AA95851.1; -; Genomic_DNA.					
DR	InterPro; IPR010656; DctM.					
DR	InterPro; IPR00252; DctM.					
DR	Pfam; PF06809; DctM; 1.					
DR	Pfam; PF00597; DctM; 1.					
RW	Complete proteome.					
SQ	SEQUENCE 441 AA; 48056 MW; 8E59B0A462757858 CRC64;					
Query Match						
Best Local Similarity		56.2%;	Score 50;	DB 2;	Length 441;	
Matches		8;	Conservative	1;	Mismatches	2;
					Indels	0;
					Gaps	0;
RESULT 2						
ID	OSYQ86_NOCFA	PRELIMINARY;	PRT;	208	AA.	
AC	OSYQ86;					
DT	25-OCT-2004 (TREMBlrel. 28, Created)					
DT	25-OCT-2004 (TREMBlrel. 28, Last sequence update)					
DT	25-OCT-2004 (TREMBlrel. 28, Last annotation update)					
DE	Hypothetical protein.					
GN	OrderedLocustNames=nfa48030;					
OS	Nocardia farcinica.					

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Nocardia.
OC NCBI_TaxID=37329;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IFM 10152;
RX PubMed=15466710; DOI=10.1073/pnas.0406410101;
RA Ishikawa J., Yamashita A., Mikami Y., Hoshino Y., Kurita H., Hotta K.,
Shiba T., Hattori M.;
RT "The complete genomic sequence of Nocardia farcinica IFM 10152.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).
DR EMBL; AP006618; BAD59655.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 208 AA; 22565 MW; EBE3243D9E52094E CRC64;

Query Match 55.1%; Score 49; DB 2; Length 208;
Best Local Similarity 46.7%; Pred. No. 16;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 EPDMLMGDRGALD 15
DB 111 DPDMYMLNRDRIDV 125
|||||:|:|:|

RESULT 3
Q5N4J9 SYNTP6 PRELIMINARY; PRT; 405 AA.
AC Q5N4J9;
DT 01-FEB-2005 (TRENBLrel. 29, Created)
DT 01-FEB-2005 (TRENBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)
DE Sun protein.
GN Name=sun; OrderedLocustNames=svC0580.d;
OS Synchococcus sp. (strain PCC 6301) (Anacystis nidulans).
OC Bacteria; Cyanobacteria; Chroococcales; Synchococcus.
OC NCBI_TaxID=265084;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PCC6301;
RA Sugita M.;
RT "Complete genome structure of the unicellular cyanobacterium Anacystis
nidulans 6301 (Synchococcus sp. PCC6301).";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP008231; BAD78770.1; -; Genomic_DNA.
DR GO; GO:0008649; P:RNA methyltransferase activity; IEA.
DR GO; GO:0006364; P:RNA processing; IEA.
DR InterPro; IPR004573; Fmu_mfrase.
DR InterPro; IPR001678; Fmu_NOI1/Nop2p.
DR InterPro; IPR006077; NusB_Remb_TM44.
DR InterPro; IPR006174; NusB_mfrase.
DR InterPro; IPR000051; SAM_bind.
DR Pfam; PF01189; Noli_Nop2_Fmu; 1.
DR Pfam; PF01029; NusB_1.
DR ProDom; PD005242; NusB_region; 1.
DR TIGRFAMs; TIGR00563; rmb; 1.
KW Complete proteome.
SQ SEQUENCE 405 AA; 44708 MW; 89F6C51BE86590C4 CRC64;

Query Match 55.1%; Score 49; DB 2; Length 405;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 10; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

OY 2 PDML--LWGDGRLD 14
DB 110 PDMLVQLMDRLGLD 124
|||||:|:|:|

RESULT 4
Q6H084 FREDI PRELIMINARY; PRT; 779 AA.
AC Q6H084;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Fremyella diplosiphon (Calothrix PCC 7601).
OC Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Microchaete.
OC NCBI_TaxID=1197;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FDJ3;
RX Stowe-Evans E.L., Ford J., Kehoe D.M.;
RT "Genomic DNA Microarray Analysis: Identification of New Genes
RT Regulated by Light Color in the Cyanobacterium Fremyella
RT diplosiphon.";
RL J. Bacteriol. 186:4338-4349(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FDJ3;
RA Stowe-Evans E., Ford J., Kehoe D.M.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY548438; AAT41885.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 779
SQ SEQUENCE 779 AA; 85897 MW; 67144DE6E472F0AD CRC64;

Query Match 55.1%; Score 49; DB 2; Length 779;
Best Local Similarity 77.8%; Pred. No. 60;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 EPDMLMGD 9
DB 422 EPDMLMGD 430
|||||:|:|:|

RESULT 5
Q7V3U3 PROMM PRELIMINARY; PRT; 217 AA.
AC Q7V3U3;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein precursor.
GN OrderedLocustNames=PWT2247;
OS Prochlorococcus marinus (strain MIT 9313).
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OC NCBI_TaxID=74547;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA Kocap G., Latimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA Ahlgren N.A., Ariello A., Coleman M., Hauser U., Hesse W.R.,
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation.";
RL Nature 424:1042-1047(2003).
DR EMBL; BX572101; CAE22421.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004605; F:phosphatidate cytidyltransferase activity; IEA.
DR GO; GO:0008654; F:phospholipid biosynthesis; IEA.
DR InterPro; IPR00374; PC_trans.
DR Pfam; PF01148; CMP_transf_1; 1.
KW Complete proteome; Hypothetical protein; Signal.
FT SIGNAL 21
SQ SEQUENCE 217 AA; 23832 MW; 522AA449E8033FEC CRC64;

Query Match 53.9%; Score 48; DB 2; Length 217;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 2 PDMLMGDRGAL 13
DB 139 PDMLMGDRKSI 150
|||||:|:|:|

RESULT 6

Q8BJF9 SHEON

ID Q8BJF9 SHEON PRELIMINARY; PRT; 262 AA.

AC Q8BJF9;

DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE Hypothetical protein S00508.

GN OrderedLocustNames=S00508;

OS Shewanella oneidensis.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;

OC Shewanellaceae; Shewanella.

OX NCBI_Taxid=70863;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=MR-1;

RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt.749;

RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gallos E.J., Nelson W.C.,

RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Mehe B.A.,

RA Clayton R.A., Meyer T., Tespin A., Scott J., Beanan M.J.,

RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,

RA Halt D.H., Kolonay J.F., Madupu R., Peterson J.D., Unayam L.A.,

RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Imprial M.,

RA Lee K., Barry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,

RA Uterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,

RA Venter J.C., Neilson K.H., Fraser C.M.;

RT "Genome sequence of the dissimilatory metal ion-reducing bacterium

RT Shewanella oneidensis."

RL Nat. Biotechnol. 20:1118-1123(2002).

DR EMBL; AB015498; AAN53589.1; -; Genomic_DNA.

DR TIGR; S00508; -;

KW Complete proteome.

SQ SEQUENCE 262 AA; 29556 MW; 5E5E6EFD52DC44C CRC64;

Query Match 53.9%; Score 48; DB 2; Length 262;

Best Local Similarity 61.5%; Pred. No. 29;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 PDWLWMDRGALD 14

DB 58 PDWLWMDRGALD 70

RESULT 7

Q55S50 CRYNE

ID Q55S50 CRYNE PRELIMINARY; PRT; 426 AA.

AC Q55S50;

DT 13-SEP-2005 (TREMBLrel. 31, Created)

DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)

DE Hypothetical protein.

GN ORFNames=CNB1140;

OS Cryptococcus neoformans var. neoformans B-3501A.

OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;

OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.

OX NCBI_Taxid=283643;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=B-3501A;

RA Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,

RA Wicks B.L., Fu J., Davis R.W.;

RT "Cryptococcus neoformans serotype D sequencing."

RL Submitted (JUL-2004) to the EMBL/Genbank/DBJ databases.

CC -! CAUTION: The sequence shown here is derived from an

CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

DR EMBL; AA01000024; BA020751.1; -; Genomic_DNA.

KW Hypothetical protein.

SQ SEQUENCE 426 AA; 47024 MW; A0F8D1F268A28310 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 426;

Best Local Similarity 53.3%; Pred. No. 47;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EPDWLWMDRGALDV 15

DB 328 KPDIWVWGRGALDL 342

RESULT 8

Q9S4Z3 SALEN

ID Q9S4Z3 SALEN PRELIMINARY; PRT; 448 AA.

AC Q9S4Z3;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE Hypothetical protein (Fragment).

OS Salmoneella enteritidis.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Salmoneella.

OX NCBI_Taxid=592;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=S1400.

RX MEDLINE=99377131; PubMed=10447888;

RA Pattery T., Hernalsteens J.-P., De Greve H.;

RT "Identification and molecular characterization of a novel Salmoneella

RT enteritidis pathogenicity island encoding an ABC transporter."

RL Mol. Microbiol. 33:791-805(1999).

DR EMBL; AF102556; AAD51877.1; -; Genomic_DNA.

DR GO; GO:0016020; C:membrane; IEA.

DR InterPro; IPR003838; DUF214.

DR Pfam; PF02687; FtsX; 1.

KW Hypothetical protein.

FT NON_TER 1

SQ SEQUENCE 448 AA; 49706 MW; 389077E50235C42A CRC64;

Query Match 53.9%; Score 48; DB 2; Length 448;

Best Local Similarity 87.5%; Pred. No. 49;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EPDWLWNG 8

DB 408 EPDWLWNG 415

RESULT 9

Q59SA1 CANAL

ID Q59SA1 CANAL PRELIMINARY; PRT; 775 AA.

AC Q59SA1;

DT 10-MAY-2005 (TREMBLrel. 30, Created)

DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)

DE Hypothetical protein.

GN ORFNames=Ca019.10974;

OS Candida albicans SC5314.

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; mitosporic Saccharomycetales; Candida.

OX NCBI_Taxid=237561;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=SC5314;

RX PubMed=15123810; DOI=10.1073/pnas.0401648101;

RA Jones T., Federpiet N.A., Chibana H., Dungan J., Kalman S.,

RA Magee B.B., Newport G., Thorensen Y.R., Agabian N., Magee P.T.,

RA Davis R.W., Scherer S.;

RT "The diploid genome sequence of Candida albicans."

RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=SC5314;

RA Dungan J., Kuo A., Newport G., Ian C.-Y., Iijima C., Adegbola O.,

RA Roberts J., Perison K., Donnelly S., Favoreto S., Tzung K.-W.,

RA Jones T., Scherer S., Agabian N.;

RT "Annotation of the Genome of *Candida albicans*.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAC001000154; EAK93359.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 775 AA; 88474 MW; 685118C6B2C914A8 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 775;
Best Local Similarity 54.5%; Pred. No. 86;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PDMLMGDRGA 12
Db 718 PEMAVWGSQGA 728

RESULT 10
Q8GM13_STRGL PRELIMINARY; PRT; 784 AA.
AC Q8GM13;
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DR UvrA-like drug resistance pump.
OS Streptomyces globisporus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycetaceae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxId=1908;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C-1027;
RX MEDLINE=22171413; PubMed=12183628; DOI=10.1126/science.1072110;
RA Liu W., Christenson S.D., Standage S., Shen B.;
RL Science 297:1170-1173 (2002).
CC -! SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AY048670; AAL0654.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0016887; P:ATPase activity; IEA.
DR GO; GO:0016787; P:hydrolase activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC_transp_1like.
DR Pfam; PF00005; ABC_tran; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
KW ATP-binding; Membrane; Nucleotide-binding; Transport.
SQ SEQUENCE 784 AA; 83960 MW; DABC2D965720A5E7 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 784;
Best Local Similarity 53.8%; Pred. No. 87;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 PDMLMGDRGALD 14
Db 204 PDMQIMAKSGRLD 216

RESULT 11
Q59S70_CANAL PRELIMINARY; PRT; 793 AA.
AC Q59S70;
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DR Hypothetical protein.
GN ORFName=CaO19.3470;
OS *Candida albicans* SC5314.
OC Bacteria; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccaromycetales; Candida.
OX NCBI_TaxId=237561;

RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federpiel N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of *Candida albicans*.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dungan J., Kuo A., Newport G., Ian C.-Y., Iijima C., Adegoja O.,
RA Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
RA Jones T., Scherer S., Agabian N.;
RT "Annotation of the genome of *Candida albicans*.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAC001000155; EAK93328.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 793 AA; 90808 MW; 870A0A0508ADF827 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 793;
Best Local Similarity 54.5%; Pred. No. 88;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PDMLMGDRGA 12
Db 735 PEMAVWGSQGA 745

RESULT 12
Q8ZR90_SALTY PRELIMINARY; PRT; 804 AA.
AC Q8ZR90;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Putative inner membrane protein.
GN Name=ybbp; OrderedlocusNames=STM0508;
OS *Salmonella typhimurium*.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; *Salmonella*.
OX NCBI_TaxId=602;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=LT;
RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
LT2.";
RL Nature 413:852-856 (2001).
DR EMBL; AB008719; AAL19462.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR003838; DUF214.
DR Pfam; PF02687; FtsX; 2.
KW Complete proteome.
SQ SEQUENCE 804 AA; 88772 MW; 72A29069A7021F11 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 804;
Best Local Similarity 87.5%; Pred. No. 89;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EPDMLMG 8
Db 764 EPDMRLMG 771

Query Match 53.9%; Score 48; DB 2; Length 804;
Best Local Similarity 87.5%; Pred. No. 89;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 13
 06ZD22_ORYSA PRELIMINARY; PRT; 527 AA.
 ID Q6ZD22_ORYSA PRELIMINARY; PRT; 527 AA.
 AC Q6ZD22;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DE Hypothetical protein P0507H12.22.
 GN Name=P0507H12.22;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 CX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC
 clone: P0507H12."
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF04338; BAC83511.1; -; Genomic_DNA.
 DR Gramene; Q6ZD22; -;
 DR GO; GO:0004519; F:endonuclease activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0006281; P:DNA repair; IEA.
 DR InterPro; IPR004843; M:pesterase.
 DR Pfam; PF00149; Metallophos; 1.
 DR Hypothetical protein.
 SQ SEQUENCE 527 AA; 61478 MW; 265BE1451BC92EB6 CRC64;

Query Match 53.4%; Score 47.5; DB 2; Length 527;
 Best Local Similarity 50.0%; Pred. No. 70;
 Matches 9; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY 1 EPPWLL--WGDGALDV 15
 ||:||:||||:|
 DB 86 EPPWLLDWYWGDKGTGTV 103

RESULT 14
 06JH28_HUMAN PRELIMINARY; PRT; 61 AA.
 ID Q6JH28_HUMAN PRELIMINARY; PRT; 61 AA.
 AC Q6JH28;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DE HCV-E2 binding protein 1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Zhang J., Cheng J., Wang L., Shao Q., Lu Y., Chen T., Hong Y.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY459290; AAR23235.1; -; mRNA.
 SQ SEQUENCE 61 AA; 6607 MW; 4E162AA344E7A56 CRC64;

Query Match 52.8%; Score 47; DB 2; Length 61;
 Best Local Similarity 87.5%; Pred. No. 9.3;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 WLLMGDRG 11
 |||||
 DB 46 WLLMGSRG 53

RESULT 15
 07UG34_RHOBA PRELIMINARY; PRT; 364 AA.
 ID 07UG34_RHOBA PRELIMINARY; PRT; 364 AA.
 AC 07UG34;

DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=RB8157;
 OS Rhodospirillum rubrum.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Pirellula.
 CX NCBI_TaxID=117;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA STRAIN=1;
 RC MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Heilmann K., Rabus R.,
 RA Schlesner H., Amann R., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.
 strain 1."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
 DR EMBL; BX294147; CAD78495.1; -; Genomic DNA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 364 AA; 40878 MW; 2284324F0722E6AB CRC64;

Query Match 52.8%; Score 47; DB 2; Length 364;
 Best Local Similarity 58.3%; Pred. No. 57;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 DWLLMGDRGALD 14
 |||||:|
 DB 162 DWLLMGDRGALD 173

Search completed: December 4, 2005, 04:52:25
 Job time : 139.875 secs

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OM protein - protein search, using sw model

Run on: December 4, 2005, 03:59:51 ; Search time 32.1875 Seconds
(without alignments)
38.528 Million cell updates/sec

Title: US-10-632-706-197
Perfect score: 89
Sequence: 1 EPDWLWMDRGALDV 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

1: Issued Patents AA: *
2: /cgn2_6/ptodata/1/1aa/5 COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6 COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/H_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PCUS_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/RE_COMB.pep: *
7: /cgn2_6/ptodata/1/1aa/Backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	53.9	229	2	US-09-489-039A-12532
2	45	50.6	614	2	US-09-543-681A-7066
3	44	49.4	80	2	US-09-248-796A-22630
4	43	48.3	345	2	US-09-303-518D-194
5	43	48.3	383	2	US-09-303-518D-196
6	43	48.3	638	2	US-09-949-016-9984
7	43	48.3	732	2	US-09-902-540-13627
8	42.5	47.8	320	2	US-09-252-991A-18301
9	42	47.2	174	2	US-09-854-133-426
10	42	47.2	388	1	US-08-290-448A-80
11	42	47.2	388	1	US-08-290-448A-80
12	42	47.2	388	1	US-08-175-069A-80
13	42	47.2	388	2	US-08-461-939B-80
14	42	47.2	388	2	US-08-464-000-80
15	42	47.2	493	2	US-09-489-039A-12903
16	41	46.1	588	4	PCT-US95-13749-4
17	41	46.1	611	2	US-09-543-681A-7066
18	41	46.1	884	2	US-09-248-796A-20574
19	40.5	45.5	392	2	US-08-311-731A-29
20	40	44.9	497	2	US-09-252-991A-27798
21	40	44.9	497	2	US-09-489-039A-12027
22	40	44.9	576	2	US-09-367-206-1
23	40	44.9	576	2	US-09-367-206-21
24	40	44.9	576	2	US-09-367-206-22
25	40	44.9	576	2	US-09-367-206-23
26	40	44.9	576	2	US-09-298-404-1
27	40	44.9	576	2	US-09-298-404-21

28	40	44.9	576	2	US-09-298-404-22	Sequence 22, Appl
29	40	44.9	576	2	US-09-298-404-23	Sequence 23, Appl
30	40	44.9	776	2	US-09-155-396-3	Sequence 3, Appl
31	39	43.8	113	1	US-08-321-625-44	Sequence 44, Appl
32	39	43.8	13	2	US-09-181-083-44	Sequence 44, Appl
33	39	43.8	13	2	US-09-750-754-44	Sequence 272, Appl
34	39	43.8	93	2	US-09-072-596-72	Sequence 272, Appl
35	39	43.8	93	2	US-09-072-967-277	Sequence 277, Appl
36	39	43.8	93	2	US-10-193-002-272	Sequence 277, Appl
37	39	43.8	93	2	US-10-084-843-277	Sequence 14417, A
38	39	43.8	141	2	US-09-902-540-14417	Sequence 45277, A
39	39	43.8	170	2	US-09-270-767-45277	Sequence 7558, Ap
40	39	43.8	194	2	US-09-489-039A-7558	Sequence 8, Appl
41	39	43.8	226	2	US-09-004-731-8	Sequence 8, Appl
42	39	43.8	226	2	US-08-749-699-8	Sequence 8, Appl
43	39	43.8	226	2	US-09-004-729-8	Sequence 8, Appl
44	39	43.8	258	2	US-09-134-000C-5594	Sequence 5594, Ap
45	39	43.8	286	2	US-09-248-796A-23020	Sequence 23020, A

ALIGNMENTS

```
RESULT 1
US-09-489-039A-12532
Sequence 12532, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12532
LENGTH: 229
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12532

Query Match      53.9%; Score 48; DB 2; Length 229;
Best Local Similarity 57.1%; Pred. NO. 7.8;
Matches      8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      1 EPDWLWMDRGALD 14
Db      32 ERSWKMGDRFAID 45

RESULT 2
US-09-543-681A-7066
Sequence 7066, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7066
LENGTH: 614
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-7066

Query Match      50.6%; Score 45; DB 2; Length 614;
```

Best Local Similarity 64.3%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Cy 1 EPDWLMDRGALD 14
Db 452 EDGWLRTGDAGALD 465

RESULT 3
US-09-248-796A-22630
; Sequence 22630, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 22630
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-22630

Query Match 49.4%; Score 44; DB 2; Length 80;
Best Local Similarity 54.5%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Cy 2 PDWLMGDRGA 12
Db 12 PDMAVMSQWA 22

RESULT 4
US-09-303-518D-194
; Sequence 194, Application US/09303518D
; Patent No. 6914131
; GENERAL INFORMATION:
; APPLICANT: Scariato, Vincenzo
; APPLICANT: Masiagnani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Neisserial Antigens
; FILE REFERENCE: CHIR0160
; CURRENT APPLICATION NUMBER: US/09/303,518D
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1098
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 194
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-09-303-518D-194

Query Match 48.3%; Score 43; DB 2; Length 345;
Best Local Similarity 70.0%; Pred. No. 72;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 2 PDWLMGDRG 11
Db 183 PEMLLFGYRG 192

RESULT 5
US-09-303-518D-196
; Sequence 196, Application US/09303518D

; Patent No. 6914131
; GENERAL INFORMATION:
; APPLICANT: Scariato, Vincenzo
; APPLICANT: Masiagnani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Neisserial Antigens
; FILE REFERENCE: CHIR0160
; CURRENT APPLICATION NUMBER: US/09/303,518D
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1098
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 196
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-303-518D-196

Query Match 48.3%; Score 43; DB 2; Length 383;
Best Local Similarity 70.0%; Pred. No. 81;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 2 PDWLMGDRG 11
Db 181 PEMLLFGYRG 190

RESULT 6
US-09-949-016-9984
; Sequence 9984, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9984
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9984

Query Match 48.3%; Score 43; DB 2; Length 638;
Best Local Similarity 85.7%; Pred. No. 1,4402;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 EPDWLW 7
Db 558 EPDWLW 564

RESULT 7
US-09-902-540-13627
; Sequence 13627, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 13627
LENGTH: 732
TYPE: PRT
ORGANISM: Myxococcus xanthus
US-09-902-540-13627

Query Match 48.3%; Score 43; DB 2; Length 732;
Best Local Similarity 63.6%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 WLMGDRALD 14
|||
Db 126 WLMGTRRAE 136

RESULT 8
US-09-252-991A-18301
Sequence 18301, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18301
LENGTH: 320
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18301

Query Match 47.8%; Score 42.5; DB 2; Length 320;
Best Local Similarity 66.7%; Pred. No. 79;
Matches 10; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 2 PDWLMGDRG-ALDV 15
|||
Db 254 PTLWMGDRDRLDV 268

RESULT 9
US-09-854-133-426
Sequence 426, Application US/09854133
Patent No. 6759508
GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamadh, Raedoh
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 426
LENGTH: 174
TYPE: PRT
ORGANISM: Homo sapiens
US-09-854-133-426

Query Match 47.2%; Score 42; DB 2; Length 174;
Best Local Similarity 70.0%; Pred. No. 49;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EPDWLMGDR 10
|||
Db 124 DPCHLMGDR 133

RESULT 10
US-08-290-448A-80
Sequence 80, Application US/08290448A
Patent No. 5676954
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,448A
FILING DATE: August 15, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandreagouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-290-448A-80

Query Match 47.2%; Score 42; DB 1; Length 388;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 EPDWLMGDRALDV 15
|||
Db 323 EPDMTMMRTQNDV 337

RESULT 11
US-08-290-448A-80
Sequence 80, Application US/08290448A
Patent No. 5698204
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn

APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,448A
FILING DATE: August 15, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-290-448A-80

Query Match 47.2%; Score 42; DB 1; Length 388;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 EPPWLMDRGALDV 15
||:|:|:|:|:|:|
Db 323 EPEWMTWNRQNDV 337

RESULT 12
US-08-175-069A-80
Sequence 80, Application US/08175069A
Patent No. 5776761
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,069A
FILING DATE: December 29, 1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-175-069A-80

Query Match 47.2%; Score 42; DB 1; Length 388;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 EPPWLMDRGALDV 15
||:|:|:|:|:|:|
Db 323 EPEWMTWNRQNDV 337

RESULT 13
US-08-461-939B-80
Sequence 80, Application US/08461939B
Patent No. 6335019
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Methods For Treating Sensitivity To A
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,939B
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/464,000
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/290,448
FILING DATE: 15-AUG-1994
APPLICATION NUMBER: US 07/529,951
FILING DATE: 29-MAY-1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: 17-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CNDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 80:

SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-939B-80

Query Match 47.2% Score 42; DB 2; Length 388;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EPDWLWMDRGALDV 15
|||:|||||
Db 323 EPEWMTWMTQNDV 337

RESULT 14
US-08-464-000-80
Sequence 80, Application US/08464000
Patent No. 6335020
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic peptides from Ragweed pollen
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,000
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/290,448
FILING DATE: 15-AUG-1994
APPLICATION NUMBER: US 07/529,951
FILING DATE: 29-MAY-1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: 17-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IM1-018CN2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-000-80

Query Match 47.2% Score 42; DB 2; Length 388;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EPDWLWMDRGALDV 15
|||:|||||
Db 323 EPEWMTWMTQNDV 337

RESULT 15
US-09-489-039A-12903
Sequence 12903, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12903
LENGTH: 493
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12903

Query Match 47.2% Score 42; DB 2; Length 493;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 WILWMDRGAL 13
|||:|||||
Db 463 WILWMDRGAL 472

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Job time : 33.1875 secs

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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:07:28 ; Search time 107.5 Seconds
(without alignments)
58.302 Million cell updates/sec

Title: US-10-632-706-197

Perfect score: 89

Sequence: 1 EPDWLWMDRGALDV 15

Scoring table: BLOSUM62

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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	89	100.0	15	US-10-632-706-130	Sequence 130, App
3	89	100.0	15	US-10-632-706-131	Sequence 131, App
4	89	100.0	15	US-10-632-706-194	Sequence 194, App
5	89	100.0	15	US-10-632-706-197	Sequence 197, App
6	89	100.0	15	US-10-632-706-200	Sequence 200, App
7	89	100.0	15	US-10-632-706-203	Sequence 203, App
8	89	100.0	15	US-10-632-706-203	Sequence 203, App
9	89	100.0	15	US-10-632-706-203	Sequence 203, App
10	89	100.0	15	US-10-632-706-203	Sequence 203, App
11	89	100.0	15	US-10-632-706-203	Sequence 203, App
12	89	100.0	15	US-10-632-706-203	Sequence 203, App
13	89	100.0	15	US-10-632-706-203	Sequence 203, App
14	89	100.0	15	US-10-632-706-203	Sequence 203, App
15	89	100.0	15	US-10-632-706-203	Sequence 203, App
16	89	100.0	15	US-10-632-706-203	Sequence 203, App
17	89	100.0	15	US-10-632-706-203	Sequence 203, App
18	89	100.0	15	US-10-632-706-203	Sequence 203, App
19	89	100.0	15	US-10-632-706-203	Sequence 203, App
20	89	100.0	15	US-10-632-706-203	Sequence 203, App
21	89	100.0	15	US-10-632-706-203	Sequence 203, App
22	89	100.0	15	US-10-632-706-203	Sequence 203, App
23	89	100.0	15	US-10-632-706-203	Sequence 203, App
24	89	100.0	15	US-10-632-706-203	Sequence 203, App
25	89	100.0	15	US-10-632-706-203	Sequence 203, App
26	89	100.0	15	US-10-632-706-203	Sequence 203, App
27	89	100.0	15	US-10-632-706-203	Sequence 203, App

28	42.5	47.8	315	4	US-10-282-122A-43588	Sequence 43588, A
29	42	47.2	77	3	US-09-764-847-922	Sequence 922, App
30	42	47.2	77	4	US-10-092-154-922	Sequence 922, App
31	42	47.2	116	4	US-10-424-599-206981	Sequence 206981, App
32	42	47.2	131	3	US-09-864-408A-4566	Sequence 4566, App
33	42	47.2	154	4	US-10-312-354-426	Sequence 426, App
34	42	47.2	174	3	US-09-738-973-426	Sequence 426, App
35	42	47.2	174	3	US-09-854-133-426	Sequence 426, App
36	42	47.2	174	4	US-10-144-649A-426	Sequence 426, App
37	42	47.2	175	5	US-10-450-763-31629	Sequence 31629, A
38	42	47.2	198	4	US-10-767-701-34131	Sequence 34131, A
39	42	47.2	211	5	US-10-450-763-37978	Sequence 37978, A
40	42	47.2	245	4	US-10-437-963-108592	Sequence 108592, A
41	42	47.2	275	4	US-10-425-114-66625	Sequence 66625, A
42	42	47.2	363	4	US-10-282-122A-50322	Sequence 50322, A
43	42	47.2	380	4	US-10-369-493-20944	Sequence 20944, A
44	42	47.2	397	3	US-09-847-208-17	Sequence 17, App
45	42	47.2	397	5	US-10-809-689-97	Sequence 97, App

ALIGNMENTS

```
RESULT 1
US-10-632-706-129
; Sequence 129, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT FILING DATE: 2003-08-01
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 129
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-129
Query Match 100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 EPDWLWMDRGALDV 15
Db 1 EPDWLWMDRGALDV 15
RESULT 2
US-10-632-706-130
; Sequence 130, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT FILING DATE: 2003-08-01
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
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; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 130
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-130

Query Match      100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EPDWLWMDRGALDV 15
Db      1 EPDWLWMDRGALDV 15

RESULT 3
US-10-632-706-131
; Sequence 131, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 131
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-131

Query Match      100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EPDWLWMDRGALDV 15
Db      1 EPDWLWMDRGALDV 15

RESULT 4
US-10-632-706-194
; Sequence 194, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 194
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-194

Query Match      100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EPDWLWMDRGALDV 15
Db      1 EPDWLWMDRGALDV 15

RESULT 5
US-10-632-706-197
; Sequence 197, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 197
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-197

Query Match      100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EPDWLWMDRGALDV 15
Db      1 EPDWLWMDRGALDV 15

RESULT 6
US-10-632-706-200
; Sequence 200, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: MARKS, JAMES D.
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 200
; LENGTH: 15
; TYPE: PRT
```

ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: single chain antibody fragment
US-10-632-706-200

Query Match 100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EPPWLWMDRGALDV 15
Db 1 EPPWLWMDRGALDV 15

RESULT 7
US-10-632-706-203
Sequence 203, Application US/10632706
Publication No. US20040175385A1
GENERAL INFORMATION:
APPLICANT: MARKS, JAMES D.
APPLICANT: AMERSOORER, PETER
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
FILE REFERENCE: 407T-895120US
CURRENT APPLICATION NUMBER: US/10/632,706
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US 60/400,721
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 09/144,806
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 203
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: single chain antibody fragment
US-10-632-706-203

Query Match 84.3%; Score 75; DB 4; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00033;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EPPWLWMDRGALDV 15
Db 1 EPPWLWMDRGALDV 15

RESULT 8
US-10-450-763-50690
Sequence 50690, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 50690
LENGTH: 334
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN

LOCATION: (267)..(320)
OTHER INFORMATION: Sodium:neurotransmitter symporter family proteins domain
OTHER INFORMATION: identified by eMATRIX, accession number BL00610D, p-value=2.000e-
OTHER INFORMATION: 25, raw score of 20.97
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (44)..(307)
OTHER INFORMATION: Sodium:neurotransmitter symporter family domain identified by
OTHER INFORMATION: Pfam, accession name SNF_E-value=2e-76, Pfam score of 267.3
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(334)
OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-50690

Query Match 57.3%; Score 51; DB 5; Length 334;
Best Local Similarity 53.3%; Pred. No. 21;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy 1 EPPWLWMDRGALDV 15
Db 263 KPDMSSWPGSGWIDV 277

RESULT 9
US-10-634-548-27
Sequence 27, Application US/10634548
Publication No. US20040045051A1
GENERAL INFORMATION:
APPLICANT: No. US20040045051A1, Susan R
APPLICANT: Lincoln, Kim
APPLICANT: Abad, Mark Scott
APPLICANT: Ellers, Robert
APPLICANT: Hartsuyker, Karen Kindle
APPLICANT: Hirschberg, Joseph
APPLICANT: Karunanandaa, Balasubramanian
APPLICANT: Moshiri, Farhad
APPLICANT: Stein, Joshua C.
APPLICANT: Valentin, Henry B.
APPLICANT: Venkatesh, Tyamagondlu V.
TITLE OF INVENTION: Tocopherol biosynthesis related genes and used thereof
FILE REFERENCE: Ren-01-125
CURRENT APPLICATION NUMBER: US/10/634,548
CURRENT FILING DATE: 2003-08-05
PRIOR APPLICATION NUMBER: US 60/400,689
PRIOR FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn version 3.2
SEQ ID NO 27
LENGTH: 201
TYPE: PRT
ORGANISM: Prochlorococcus marinus-MIT9313
US-10-634-548-27

Query Match 53.9%; Score 48; DB 4; Length 201;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PDMWLWMDRGAL 13
Db 123 PDMWLWMDRGALSI 134

RESULT 10
US-10-159-257A-160
Sequence 160, Application US/10159257A
Publication No. US20040161828A1
GENERAL INFORMATION:
APPLICANT: SHEN, BEN
APPLICANT: LIU, WEN
APPLICANT: CHRISTENSON, STEVEN D.
APPLICANT: STANDAGE, SCOTT
TITLE OF INVENTION: GENE CLUSTER FOR PRODUCTION OF THE ENEDIYNE ANTITUMOR

```

; TITLE OF INVENTION: ANTIBIOTIC C-1027
; FILE REFERENCE: 407T-896020US
; CURRENT APPLICATION NUMBER: US/10/159,257A
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 09/478,188
; PRIOR FILING DATE: 2000-01-05/115,434
; PRIOR APPLICATION NUMBER: 60/115,434
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 160
; LENGTH: 775
; TYPE: PRT
; ORGANISM: Streptomyces globisporus
; FEATURE:
; OTHER INFORMATION: orf(-1)
US-10-159-257A-160

Query Match          53.9%; Score 48; DB 4; Length 775;
Best Local Similarity 53.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      2  PDMWLWMDRGALD 14
DB      195 PDMQIMAKSGRLD 207

RESULT 11
US-10-437-963-134365
; Sequence 134365, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bardazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO: 134365
; LENGTH: 992
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_36146C.1.pep
US-10-437-963-134365

Query Match          53.4%; Score 47.5; DB 4; Length 992;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY      1  BPDWL---WGDGALDV 15
DB      551 BPNWLLDMWGDKTGTNV 568

RESULT 12
US-10-450-763-52883
; Sequence 52883, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
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; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO: 52883
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(455)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-52883

Query Match          52.8%; Score 47; DB 5; Length 455;
Best Local Similarity 53.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1  BPDWLWMDRGAL 13
DB      93 EQNWLMWCRGVM 105

RESULT 13
US-10-369-493-12420
; Sequence 12420, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO: 12420
; LENGTH: 904
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
US-10-369-493-12420

Query Match          52.8%; Score 47; DB 4; Length 904;
Best Local Similarity 70.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      4  WLWGDRCAL 13
DB      460 WLWGDKTSL 469

RESULT 14
US-10-425-115-240160
; Sequence 240160, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
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; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 240160
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(159)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: clone ID: MRT4577_150607C.1.pep
US-10-425-115-240160
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Query Match          50.6%; Score 45; DB 4; Length 159;
Best Local Similarity 75.0%; Pred. No. 83;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      2 PDWLLMGDRGAL 13
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Db      35 PGRLLMGRRGAL 46
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RESULT 15

US-10-282-122A-68332

; Sequence 68332, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: EUTRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; PRIOR FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 68332

; LENGTH: 372

; TYPE: PRT

; ORGANISM: Pseudomonas putida

US-10-282-122A-68332

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Query Match          50.6%; Score 45; DB 4; Length 372;
Best Local Similarity 70.0%; Pred. No. 1,8e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db      221 PDWLLMTTPAG 230
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:08:08 ; Search time 4.375 Seconds
(without alignments)
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Title: US-10-632-706-197
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Published Applications AA New:*

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- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEM_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	48.3	383	6	US-10-467-657-5602
2	41	46.1	251	7	US-11-054-515-1084
3	40.5	45.5	125	6	US-10-821-234-1277
4	38.5	43.3	1075	7	US-11-174-150-34
5	38.5	42.3	1114	7	US-11-174-150-35
6	38	42.7	248	7	US-11-054-515-1679
7	38	42.7	251	7	US-11-054-515-944
8	37	41.6	344	6	US-10-967-527A-24
9	36	40.4	225	6	US-10-821-234-1116
10	36	40.4	322	6	US-10-467-657-1006
11	36	40.4	428	6	US-10-793-626-484
12	36	40.4	1857	7	US-11-057-058-60
13	36	40.4	1857	7	US-11-057-058-61
14	35.5	33.9	158	6	US-10-510-386-128
15	35.5	33.9	247	6	US-10-793-626-1466
16	35.5	33.9	344	6	US-10-821-234-923
17	35.5	33.9	380	6	US-10-624-932-20
18	35	33.3	239	6	US-10-957-569-54
19	35	33.3	350	6	US-10-467-657-5824
20	35	33.3	401	6	US-10-510-386-68
21	35	33.3	530	6	US-10-980-388-62
22	35	33.3	551	6	US-10-793-626-1668
23	34.5	38.8	1613	7	US-11-108-528-84
24	34.5	38.8	1613	7	US-11-108-528-86
25	34	38.2	251	7	US-11-054-515-1079

26	34	38.2	251	7	US-11-054-515-1793	Sequence 1793, Ap
27	34	38.2	253	7	US-11-015-546A-2	Sequence 2, Appl
28	34	38.2	253	7	US-11-054-515-1069	Sequence 1069, Ap
29	34	38.2	269	7	US-11-015-546A-10	Sequence 10, Appl
30	34	38.2	274	7	US-11-015-546A-12	Sequence 12, Appl
31	34	38.2	486	6	US-10-821-234-1063	Sequence 1063, Ap
32	34	38.2	613	6	US-10-131-826A-190	Sequence 190, Ap
33	34	38.2	616	6	US-10-131-826A-206	Sequence 206, Ap
34	34	38.2	820	7	US-11-147-047-31	Sequence 31, Appl
35	34	38.2	2725	7	US-11-113-424-82	Sequence 52, Appl
36	33.5	37.6	137	6	US-10-821-234-882	Sequence 882, Appl
37	33.5	37.6	249	7	US-11-054-515-649	Sequence 649, Appl
38	33	37.1	91	6	US-10-467-657-1052	Sequence 1052, Ap
39	33	37.1	177	6	US-10-980-388-95	Sequence 95, Appl
40	33	37.1	247	7	US-11-054-515-1307	Sequence 1307, Ap
41	33	37.1	248	7	US-11-054-515-877	Sequence 877, Appl
42	33	37.1	248	7	US-11-054-515-953	Sequence 953, Appl
43	33	37.1	248	7	US-11-054-515-965	Sequence 965, Appl
44	33	37.1	248	7	US-11-054-515-980	Sequence 980, Appl
45	33	37.1	248	7	US-11-054-515-984	Sequence 984, Appl

ALIGNMENTS

```
RESULT 1
US-10-467-657-5602
; Sequence 5602, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASTIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5602
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5602

Query Match      48.3%  Score 43;  DB 6;  Length 383;
Best Local Similarity 70.0%  Pred. No. 3.8;
Matches          7;  Conservative 2;  Mismatches 1;  Indels 0;  Gaps 0;

Cy      2 PDWLMGDRG 11
Db      181 PFWLFGKRG 190

RESULT 2
US-11-054-515-1084
; Sequence 1084, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523p3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
```

```

? PRIOR FILING DATE: 2002-11-14
? PRIOR APPLICATION NUMBER: 60/333,469
? PRIOR FILING DATE: 2001-11-16
? PRIOR APPLICATION NUMBER: 60/340,817
? PRIOR FILING DATE: 2001-12-19
? PRIOR APPLICATION NUMBER: 09/880,748
? PRIOR FILING DATE: 2001-06-15
? PRIOR APPLICATION NUMBER: 60/299,499
? PRIOR FILING DATE: 2001-05-25
? PRIOR APPLICATION NUMBER: 60/277,319
? PRIOR FILING DATE: 2001-03-21
? PRIOR APPLICATION NUMBER: 60/276,248
? PRIOR FILING DATE: 2001-03-16
? PRIOR APPLICATION NUMBER: 60/240,816
? PRIOR FILING DATE: 2000-10-17
? Remaining Seq Application data removed - See File Wrapper or PALM
? NUMBER OF SEQ ID NOS: 3247
? SEQ ID NO 1084
? LENGTH: 251
? TYPE: PRF
? ORGANISM: Homo sapiens
? US-11-054-515-1084

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Query Match	46.1%	Score 41;	DB 7;	Length 251;
Best Local Similarity	46.2%	Pred. No. 5.1;		
Matches	6;	Conservative	3;	Mismatches 4;
				Indels 0;
				Gaps 0;

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QY      2 PDWLLMGDRGALD 14
         |::|::|
Db      45 PEMMGWINRGGS 57
```

```

RESULT 3
US-10-821-234-1277
: Sequence 1277, Application US/10821234
: Publication No. US2005025511A1
: GENERAL INFORMATION:
: APPLICANT: Labat, Ivan
: APPLICANT: Stache-Crain, Birgit
: APPLICANT: Andarmani, Susan
: APPLICANT: Tang, Y. Tom
: TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
: FILE REFERENCE: 821A
: CURRENT APPLICATION NUMBER: US/10/821,234
: CURRENT FILING DATE: 2004-04-07
: PRIOR APPLICATION NUMBER: US 60/462,047
: PRIOR FILING DATE: 2003-04-07
: NUMBER OF SEQ ID NOS: 1704
: SOFTWARE: pc_seq_genes Version 1.0
: SEQ ID NO 1277
: LENGTH: 125
: TYPE: PRF
: ORGANISM: Homo sapiens
: US-10-821-234-1277

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Query Match	45.5%	Score 40.5;	DB 6;	Length 125;
Best Local Similarity	63.6%;	Pred. No.3.1;		
Matches	7;	Conservative	3;	Mismatches 0;
			Indels	1;
			Gaps	1

```
QY      1 EPDWLLMGDRG 11
          :|||:|:||
Db      101 DPDWLI-GERG 110
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RESULT 4
US-11-174-150-34
Sequence 34, Application US/11174150
Publication No. US2005026074A1
GENERAL INFORMATION:
APPLICANT: Agarwal, Pankaj
APPLICANT: Murodch, Paul R.
APPLICANT: Rizvi, Safia K.
APPLICANT: Smith, Randall F.

```

1 APPLICANT: Xiang Zhaoyang
2 TITLE OF INVENTION: NOVEL COMPOUNDS
3 FILE REFERENCE: GPT0022
4 CURRENT APPLICATION NUMBER: US/11/174,150
5 CURRENT FILING DATE: 2005-07-01
6 PRIOR APPLICATION NUMBER: US/10/257,174
7 PRIOR FILING DATE: 2002-10-10
8 PRIOR APPLICATION NUMBER: PCT/US01/11797
9 PRIOR FILING DATE: 2001-04-11
10 PRIOR APPLICATION NUMBER: 60/196,603
11 PRIOR FILING DATE: 2000-04-13
12 PRIOR APPLICATION NUMBER: 60/199,417
13 PRIOR FILING DATE: 2000-04-24
14 NUMBER OF SEQ ID NOS: 48
15 SOFTWARE: FastSeq for Windows Version 3.0
16 SEQ ID NO 34
17 LENGTH: 1075
18 TYPE: PRt
19 ORGANISM: Homo sapiens
20 US-11-174-150-34

```

Query Match	43.3%;	Score 38.5;	DB 7;	Length 1075;
Best Local Similarity	53.8%;	Pred. No. 51;		
Matches	7;	Conservative	2;	Mismatches 1;
			Indels	3;
			Gaps	1;

```

QY      3 DWLLWG---DRGA 12
        : : | | | |
Db      922 EWSVWGSWYDRGA 934

```

```

US-11-174-150-35
RESULT 5
Sequence 35, Application US/11174,150
Publication NO. US20050260714A1
GENERAL INFORMATION:
APPLICANT: Agarwal, Pankaj
APPLICANT: Murdoch, Paul R.
APPLICANT: Rizvi, Safia K.
APPLICANT: Smith, Randall F.
APPLICANT: Xiang, Zhaoxing
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GPO0022
CURRENT APPLICATION NUMBER: US/11/174,150
CURRENT FILING DATE: 2005-07-01
PRIOR APPLICATION NUMBER: US/10/257,174
PRIOR FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: PCT/US01/11797
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/196,603
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 60/199,417
PRIOR FILING DATE: 2000-04-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FASTSEQ for Windows Version 3.0.0
SEQ ID NO 35
LENGTH: 1114
TYPE: PRM
ORGANISM: Homo sapiens
US-11-174-150-35

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Query Match	43.3%	Score 38.5;	DB 7;	Length 1114;
Best Local Similarity	53.8%	Pred. No. 53;		
Matches	7;	Conservative	2;	Mismatches 1;
			Indels 3;	Gaps 1

```
QY      3 DWLWG---DRGA 12
      :|:| | | |
Db      961 EWSVWGSWYDRGA 973
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RESULT 6
US-11-054-515-1679
; Sequence 1679, Application US/11054515
; Publication No. US20050255532A1

```

; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23p3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1679
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1679

Query Match          42.7%; Score 38; DB 7; Length 248;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Cy      1  EPDWLWMDRGALD 14
      |||:|:|:|:|
Db      44  EPEWGWINGSGD 57

RESULT 7
US-11-054-515-944
; Sequence 944, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23p3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1679
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1679
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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 944
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-944

Query Match          42.7%; Score 38; DB 7; Length 251;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Cy      1  EPDWLWMDRGALD 14
      |||:|:|:|:|
Db      44  EPEWGWINGSGD 57

RESULT 8
US-10-967-527A-24
; Sequence 24, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnf14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; PRIOR FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 344
; TYPE: PRT
; ORGANISM: mus musculus
US-10-967-527A-24

Query Match          41.6%; Score 37; DB 6; Length 344;
Best Local Similarity 83.3%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy      2  PDWLLW 7
      |||||
Db      3  PSWLLW 8

RESULT 9
US-10-821-234-1116
; Sequence 1116, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1116
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1116

Query Match          40.4%; Score 36; DB 6; Length 225;
```

Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 WLMGDRG 11
|:|:|:|
Db 74 WVRWGRG 81

RESULT 10

US-10-467-657-1006
; Sequence 1006, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 1006
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1006

Query Match 40.4%; Score 36; DB 6; Length 322;
Best Local Similarity 63.6%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PDMWLMGDRGA 12
|:|:|:|
Db 251 PDMFLVLDRSA 261

RESULT 11

US-10-793-626-484
; Sequence 484, Application US/10793626
; Publication No. US20050253478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 484
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-484

Query Match 40.4%; Score 36; DB 6; Length 428;
Best Local Similarity 62.5%; Pred. No. 50;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 WGDGRGALD 14
|:|:|:|
Db 333 WGDKGVD 340

RESULT 12
US-11-057-058-60
; Sequence 60, Application US/11057058
; Publication No. US20050244400A1
; GENERAL INFORMATION:
; APPLICANT: Lebowitz, Jonathan
; APPLICANT: Maza, John
; TITLE OF INVENTION: ACID ALPHA-GLUCOSIDASE AND FRAGMENTS THEREOF
; FILE REFERENCE: SYM-011
; CURRENT APPLICATION NUMBER: US/11/057,058
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: US 60/543,812
; PRIOR FILING DATE: 2004-02-10
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 60
; LENGTH: 1857
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-057-058-60

Query Match 40.4%; Score 36; DB 7; Length 1857;
Best Local Similarity 45.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 WLMGDRGALD 14
|:|:|:|
Db 1749 WLFMDGQSID 1759

RESULT 13
US-11-057-058-61
; Sequence 61, Application US/11057058
; Publication No. US20050244400A1
; GENERAL INFORMATION:
; APPLICANT: Lebowitz, Jonathan
; APPLICANT: Maza, John
; TITLE OF INVENTION: ACID ALPHA-GLUCOSIDASE AND FRAGMENTS THEREOF
; FILE REFERENCE: SYM-011
; CURRENT APPLICATION NUMBER: US/11/057,058
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: US 60/543,812
; PRIOR FILING DATE: 2004-02-10
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
; LENGTH: 1857
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-057-058-61

Query Match 40.4%; Score 36; DB 7; Length 1857;
Best Local Similarity 45.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 WLMGDRGALD 14
|:|:|:|
Db 1749 WLFMDGQSID 1759

RESULT 14
US-10-510-386-128
; Sequence 128, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294,204-US
; CURRENT APPLICATION NUMBER: US/10/510,386

; CURRENT FILING DATE: 2004-10-04
 ; NUMBER OF SEQ ID NOS: 248
 ; SOFTWARE: Patent version 3.3
 ; SEQ ID NO 128
 ; LENGTH: 158
 ; TYPE: PRT
 ; ORGANISM: Bacillus licheniformis
 US-10-510-386-128

Query Match 39.9%; Score 35.5; DB 6; Length 158;
 Best Local Similarity 72.7%; Pred. No. 23;
 Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 5 LLM-GDRGALD 14
 DB 65 LYMIGDRGKLD 75

RESULT 15
 US-10-793-626-1466
 ; Sequence 1466, Application US/10793626
 ; Publication No. US20050253478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PUS480US
 ; CURRENT APPLICATION NUMBER: US/10/793,626
 ; FILING DATE: 2004-03-04
 ; PRIOR APPLICATION NUMBER: 60/164,258
 ; PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: Patent Ver. 2.1
 ; SEQ ID NO 1466
 ; LENGTH: 247
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: amino acid sequence
 US-10-793-626-1466

Query Match 39.9%; Score 35.5; DB 6; Length 247;
 Best Local Similarity 63.6%; Pred. No. 35;
 Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 4 WL-LMGDRGAL 13
 DB 186 WMNLMGNV GAL 196

Search completed: December 4, 2005, 04:37:50
 Job time : 5.375 secs

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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:36 ; Search time 100.375 Seconds
(without alignments)
77.318 Million cell updates/sec

Title: US-10-632-706-198
Perfect score: 59
Sequence: 1 WGGGTTVTYSS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	59	100.0	119 2	Q9GYZ2_MOUSE
2	59	100.0	121 2	O8CGS2_MOUSE
3	59	100.0	146 1	HY21_HUMAN
4	59	100.0	147 1	HY1C_HUMAN
5	59	100.0	147 2	Q925S3_MOUSE
6	59	100.0	159 2	Q96Q80_HUMAN
7	59	100.0	170 2	Q925S2_MOUSE
8	59	100.0	218 2	Q925S1_MOUSE
9	59	100.0	241 2	Q921A6_MOUSE
10	59	100.0	348 2	Q6PYX1_HUMAN
11	59	100.0	416 2	Q9NPP6_HUMAN
12	59	100.0	472 2	Q6N089_HUMAN
13	59	100.0	573 2	O8MUJ8_HUMAN
14	59	100.0	575 2	O6P4I8_HUMAN
15	59	100.0	595 2	O8WUX4_HUMAN
16	59	100.0	597 2	Q9BU10_HUMAN
17	59	100.0	597 2	Q9BOB8_HUMAN
18	59	100.0	597 2	O6GMX5_HUMAN
19	59	100.0	606 2	O6GMW2_HUMAN
20	59	100.0	625 2	O96AA6_HUMAN
21	58	98.3	465 2	O6PUB2_MOUSE
22	58	98.3	468 2	O669W9_MOUSE
23	58	98.3	468 2	O605N9_MOUSE
24	58	98.3	471 2	O66K04_MOUSE
25	58	98.3	472 2	O6PUA7_MOUSE
26	58	98.3	473 2	O91Z05_MOUSE
27	58	98.3	476 2	O669X1_MOUSE
28	58	98.3	477 2	O58E56_MOUSE
29	58	98.3	486 2	O91Z07_MOUSE
30	58	98.3	487 2	O99K44_MOUSE
31	56	94.9	109 2	O9J175_MOUSE

32	56	94.9	111 1	HV35_MOUSE	P01804_mus musculus
33	56	94.9	114 2	O9J181_MOUSE	O9J181_mus musculus
34	56	94.9	117 2	O90XFO_MOUSE	O90XFO_mus musculus
35	56	94.9	118 1	HV39_MOUSE	P01809_mus musculus
36	56	94.9	118 2	O921C4_MOUSE	O921C4_mus musculus
37	56	94.9	120 1	HV03_MOUSE	P01747_mus musculus
38	56	94.9	121 1	HV01_MOUSE	P01745_mus musculus
39	56	94.9	134 2	O65ZR6_MOUSE	O65ZR6_mus musculus
40	56	94.9	136 1	HV15_MOUSE	P01759_mus musculus
41	56	94.9	137 1	HV11_MOUSE	P01755_mus musculus
42	56	94.9	137 1	HV46_MOUSE	P01822_mus musculus
43	56	94.9	137 2	O924R6_MOUSE	O924R6_mus musculus
44	56	94.9	139 1	HV07_MOUSE	P01751_mus musculus
45	56	94.9	140 2	O924P8_MOUSE	O924P8_mus musculus

ALIGNMENTS

```

RESULT 1
ID O9GYZ2_MOUSE PRELIMINARY; PRT; 119 AA.
AC O9GYZ2;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30 heavy
DE chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Song X.T., Feng Z.Q., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282622; AAC01452.1; -; mRNA.
DR HSSP; P01751; 1A6W.
DR SMR; O9GYZ2; 1-119.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13567 MW; BA893873FDSFA6AB CRC64;

Query Match 100.0%; Score 59; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTYSS 11
DB 109 WGGGTTVTYSS 119

RESULT 2
ID O8CGS2_MOUSE PRELIMINARY; PRT; 121 AA.
AC O8CGS2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Anti-deoxyvalenol scfv lambda heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.

```

OK NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN-BALB/c;
 RA Wang Z., Munehi K., Osawa F., Pestka J.J., Hart L.P.;
 RL Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL, AY151140; F01751; INCB.
 DR HSSP; P01751; INCB.
 DR Ensemble; ENSMUSG0000021155; Mus musculus.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 FT NON_TER 1 121
 FT NON_TER 121 121
 SQ SEQUENCE 121 AA; 13475 MW; 84P6CFA8053F5D6 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 121;
 Best Local Similarity 100.0%; Pred. No. 0.0054;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WGGGTTTVSS 11
 |||||
 Db 111 WGGGTTTVSS 121

RESULT 3

HV21_HUMAN STANDARD; PRT; 146 AA.
 AC P06331;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V-II region ARH-77 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=8520532; PubMed=3922855; DOI=10.1016/0378-1119(85)90092-7;
 RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
 RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
 RT repeat sequence in 5' flanking region."
 RL Gene 33:181-189 (1985).
 CC CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC PIR; A02101; G1HHR2.
 DR HSSP; P01825; 7FAB.
 DR SMR; P06331; 21-146.
 DR GO; GO:0005576; C:extracellular region; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KW Immunoglobulin domain; Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 1 146
 FT REGION 20 146 Ig heavy chain V-II region ARH-77.
 FT REGION 118 127 D segment.
 FT REGION 128 146 J segment.
 FT DISULFID 42 115 By similarity.
 FT NON_TER 146 146
 SQ SEQUENCE 146 AA; 16228 MW; 8D7FD5B218171F CRC64;

Query Match 100.0%; Score 59; DB 1; Length 146;
 Best Local Similarity 100.0%; Pred. No. 0.0066;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WGGGTTTVSS 11
 |||||
 Db 136 WGGGTTTVSS 146

RESULT 4

HVIC_HUMAN STANDARD; PRT; 147 AA.
 AC P01744;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ig heavy chain V-I region ND precursor (Fragments).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=83065234; PubMed=6815656;
 RA Kenten J.H., Moigaard H.V., Houghton M., Derbyshire R.B., Viney J.,
 RA Bell L.O., Gould H.J.;
 RT "Cloning and sequence determination of the gene for the human
 RT immunoglobulin epsilon chain expressed in a myeloma cell line."
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665 (1982).
 RN [2]
 RP PROTEIN SEQUENCE OF 20-147.
 RA Benrich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
 RL (In) Bach M.K. (eds.);
 RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
 RL Marcel Dekker, New York (1978).
 CC -I- MISCELLANEOUS: This epsilon chain was isolated from a myeloma
 CC protein.
 CC -I- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
 CC CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC HSSP; P01751; INCB.
 DR GO; GO:0005576; C:extracellular region; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003596; IG_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin domain;
 KW Immunoglobulin V region; Pyroglutamate carboxylic acid; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 147 Ig heavy chain V-I region ND.
 FT DOMAIN 20 131 IG-like.
 FT MOD_RES 20 20 Pyroglutamate carboxylic acid.
 FT DISULFID 41 115
 FT CONFLICT 21 21 T -> V (in Ref. 2).
 FT CONFLICT 53 54 IH -> HI (in Ref. 2).
 FT CONFLICT 67 68 VG -> GV (in Ref. 2).
 FT CONFLICT 125 125 Missing (in Ref. 2).
 FT NON_TER 147 147
 SQ SEQUENCE 147 AA; 16496 MW; 948P9F72A536CC20 CRC64;

Query Match 100.0%; Score 59; DB 1; Length 147;
 Best Local Similarity 100.0%; Pred. No. 0.0067;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WGGGTTTVSS 11

Db 137 WGGTTVTSS 147

RESULT 5

Q92553_MOUSE PRELIMINARY; PRT; 147 AA.
AC Q92553;
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE MRP3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Myrodia; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D.X., Zeng G.Y., Wang F., Xu J.R., Ren D.Q., Guo Y.H., Tian F.R.,
Yan X.J., Hou Y., Su C.Z.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
the repair of intestinal epithelium after gamma-irradiation in mice."
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
of the irradiated mice by treatment with the intestinal RNA of mice of
the same strain."
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240166; AAK3731.1; -, mRNA.
DR HSP; P01751; 1A6W.
DR SMR; Q92553; 3-139.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00406; IGV, 1_v.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;

Query Match 100.0%; Score 59; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.0067;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGTTVTSS 11
Db 111 WGGTTVTSS 121

RESULT 6
Q96QSO_HUMAN PRELIMINARY; PRT; 159 AA.
AC Q96QSO;
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE Putative matrix cell adhesion molecule-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=M.D.;
RA Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY039025; AAK82649.1; -, mRNA.
DR HSP; P01869; 1A66.
DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV, 1_v.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGTTVTSS 11
Db 139 WGGTTVTSS 149

RESULT 7

Q92552_MOUSE PRELIMINARY; PRT; 170 AA.
AC Q92552;
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE MRP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Myrodia; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D.X., Zeng G.Y., Wang F., Xu J.R., Ren D.Q., Guo Y.H., Tian F.R.,
Yan X.J., Hou Y., Su C.Z.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
the repair of intestinal epithelium after gamma-irradiation in mice."
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
of the irradiated mice by treatment with the intestinal RNA of mice of
the same strain."
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240167; AAK43732.1; -, mRNA.
DR HSP; P01751; 1A6W.
DR SMR; Q92552; 3-124.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00406; IGV, 1_v.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 170 AA; 17978 MW; 5042823CC6C10F38 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGTTVTSS 11
Db 113 WGGTTVTSS 123

RESULT 8
Q92551_MOUSE PRELIMINARY; PRT; 218 AA.
AC Q92551;
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
DE MRP5 (Fragment).
OS Mus musculus (Mouse).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN NR
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BAIB/c;
RX PubMed=1819679;
RA Cui D.X., Zeng G.Y., Wang F., Xu J.R., Ren D.Q., Guo Y.H., Tian F.R.,
RA Yan X.J., Hou Y., Su C.Z.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after gamma-irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BAIB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR HSSP; P01665; 10N2.
DR Ensembl; ENSMUSG00000058040; Mus musculus.
DR InterPro; IPR007110; 19-1like.
DR InterPro; IPR003596; 19-V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON_TER
FT SEQUENCE 218 AA; 23013 MW; 52764FA8F7982817 CRC64;
SQ
Query Match 100.0%; Score 59; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WGGGTTTVSS 11
DB 110 WGGGTTTVSS 120

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DR PIR; S26325; S26325.
DR HSSP; P01607; 1BWW.
DR Ensembl; ENSMUSG00000021155; Mus musculus.
DR InterPro; IPR007110; 19-1like.
DR InterPro; IPR003596; 19-V.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS0835; IG_LIKE; 2.
FT NON_TER
FT NON_TER
FT SEQUENCE 241 AA; 26086 MW; 0276887248B9C771 CRC64;
SQ
Query Match 100.0%; Score 59; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WGGGTTTVSS 11
DB 108 WGGGTTTVSS 118

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RESULT 9
O921A6_MOUSE PRELIMINARY; PRT; 241 AA.
AC O921A6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ant-CBA 79 single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN NR
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CBA antibody (CBA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819(1997).
RN
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91341421; PubMed=1908510; DOI=10.1084/jem.174.3.613;
RA Stark S.E., Caton A.J.;
RT "Antibodies that are specific for a single amino acid interchange in a
RT protein epitope use structurally distinct variable regions.";
RL J. Exp. Med. 174:613-624(1991).
DR EMBL; U88067; AAB84044.1; -, mRNA.
DR PIR; S19965; S19965.
DR PIR; S19967; S19967.
DR PIR; S19968; S19968.

```

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DR PIR; S26325; S26325.
DR HSSP; P01607; 1BWW.
DR Ensembl; ENSMUSG00000021155; Mus musculus.
DR InterPro; IPR007110; 19-1like.
DR InterPro; IPR003596; 19-V.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS0835; IG_LIKE; 2.
FT NON_TER
FT NON_TER
FT SEQUENCE 241 AA; 26086 MW; 0276887248B9C771 CRC64;
SQ
Query Match 100.0%; Score 59; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WGGGTTTVSS 11
DB 108 WGGGTTTVSS 118

```

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RESULT 10
O6PYX1_HUMAN PRELIMINARY; PRT; 348 AA.
AC O6PYX1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hepatitis B virus receptor binding protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RN NR
RP NUCLEOTIDE SEQUENCE.
RA Zhu N.S., Chen Y.Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY570731; AAS88328.1; -, mRNA.
DR PDB; 1T89; X-ray; A/B=--.
DR SMR; O6PYX1; 3-348.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; 19-1like.
DR InterPro; IPR003597; 19-1.
DR InterPro; IPR003006; 19_MHC.
DR Pfam; PF07654; C1-sect; 3.
DR SMART; SM00407; IGV; 3.
DR PROSITE; PS0835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KM Receptor.
FT NON_TER
FT SEQUENCE 348 AA; 38162 MW; DD96C3D7E0B5845 CRC64;
SQ
Query Match 100.0%; Score 59; DB 2; Length 348;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WGGGTTTVSS 11
DB 8 WGGGTTTVSS 18

```

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RESULT 11
O9NPP6_HUMAN PRELIMINARY; PRT; 416 AA.
AC O9NPP6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Immunoglobulin heavy chain variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.

```

```

OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Auffray C., Anseorge W., Ballabio A., Estivill X., Gibson K.,
RA Leinrich H., Poustka A., Lundberg J.;
RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Pluvineret R., Estivill X., Escarceller M., Sunoy L.;
RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AL389978; CAB97534.1; -, mRNA.
DR HSSP; P01876; IOM0.
DR SMK; Q9NPP6; 186-394.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-sec; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
FT NON_TER
SQ SEQUENCE 416 AA; 44786 MW; 8C41708BB8AB4687 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGCTVTVSS 11
Db 66 WGGCTVTVSS 76

RESULT 12
Q6N089 HUMAN
ID Q6N089 HUMAN PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686P15220.
GN Name=DKFZp686P15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Rectum tumor;
RA The German cDNA Consortium;
RA Wandut R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/Genbank/DBJ databases.
DR EMBL; BX640627; CA645781.1; -, mRNA.
DR HSSP; P01861; IAD0.
DR InterPro; IPR003599; IG_1like.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-sec; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 472;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 WGGCTVTVSS 11
Db 132 WGGCTVTVSS 142

RESULT 13
Q6WU38 HUMAN
ID Q6WU38 HUMAN PRELIMINARY; PRT; 573 AA.
AC Q6WU38;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGH domain protein.
GN Name=IGHD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo A.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshitsuki S., Carninci P., Prange C.,
RA Raha S.S., Loguélano N.A., Peters G.J., Abramson R.D., Muljaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schenck A., Schein J.E., Jones S.J.M., Matra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Director MGC Project;
RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
RN [3]
RP PROTEIN SEQUENCE.
RX PubMed=1555592;
RA Makiya R., Stigbrand T.;
RT "Placental alkaline phosphatase has a binding site for the human
RT immunoglobulin-G Fc portion.";
RL Eur. J. Biochem. 205:341-345(1992).
DR EMBL; BC021276; AA821276.1; -, mRNA.
DR PIR; S21205; S21205.
DR PIR; S30532; S30532.
DR HSSP; P18529; I18K.
DR Ensemble; ENSG00000196122; Homo sapiens.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-sec; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Immunoglobulin domain; Repeat.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;

```

Query Match 100.0%; Score 59; DB 2; Length 573;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 133 WGCITTVSS 11
1 WGCITTVSS 11
133 WGCITTVSS 143

RESULT 14
06P418 HUMAN
ID 06P418 HUMAN PRELIMINARY; PRT; 576 AA.
AC 06P418
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGH protein.
GN Name:IGHD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diciccheno L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Bikesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.T., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RA EMBL; BC063384; AAH63384.1; -, mRNA.
DR HSSP; P01820; 1A7N.
DR Ensembl; ENSG00000196122; Homo sapiens.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-sec; 1.
DR Pfam; PF00447; Ig; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 576 AA; 63364 MW; FBB97C949720F1E CRC64;

Query Match 100.0%; Score 59; DB 2; Length 576;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 WGCITTVSS 11
Db 136 WGCITTVSS 146
136 WGCITTVSS 146

RESULT 15
08WUX4 HUMAN
ID 08WUX4 HUMAN PRELIMINARY; PRT; 595 AA.
AC 08WUX4
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diciccheno L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Bikesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.T., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=89235232; PubMed=2497188;
RA Sanz I., Casali P., Thomas J.W., Nockin A.L., Capra J.D.;
RT "Nucleotide sequences of eight human natural autointibody VH regions
RT reveal apparent restricted use of VH families";
RL J. Immunol. 142:4054-4061(1989).
DR EMBL; BC019235; AAH19235.2; -, mRNA.
DR PIR; G34964; G34964.
DR HSSP; P01861; 1ADQ.
DR SMR; 08WUX4; 27-256.
DR Ensembl; ENSG00000130076; Homo sapiens.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-sec; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 595 AA; 65291 MW; 0D4B5076545714E CRC64;

Query Match 100.0%; Score 59; DB 2; Length 595;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
|||||
Db 141 WGGGTTTVSS 151

Search completed: December 4, 2005, 04:52:27
Job time : 102.375 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: December 4, 2005, 04:09:54 ; Search time 95.5625 Seconds
(Without alignments)
50.576 Million cell updates/sec

Title: US-10-632-706-127

Perfect score: 60

Sequence: 1 LATYYRFGDVL 11

Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	11	8	ADR38724 Mouse hea
2	60	100.0	11	8	ADR38725 Mouse hea
3	48	80.0	122	9	AEBA45960 Human mon
4	47	78.3	114	7	ADD28082 Lymphoma
5	47	78.3	129	7	ADD28323 Human het
6	47	78.3	134	7	ADD28237 Human het
7	47	78.3	134	9	ADVB6824 Bacillus
8	47	78.3	244	8	ADR28082 NPB poly
9	47	78.3	468	9	AEBA45853 Human mon
10	47	78.3	468	9	AEBA45853 Human mon
11	46	76.7	13	8	ADR38712 Mouse hea
12	46	76.7	21	9	ADM04816 PAPP-A im
13	46	76.7	126	9	ADZ41994 Ig H chai
14	46	76.7	140	9	ADM04810 PAPP-A im
15	45	75.0	16	9	ADM04952 PAPP-A im
16	45	75.0	21	5	ABP47057 Human Bly
17	45	75.0	21	7	ADG97884 scFV VHCD
18	45	75.0	24	9	ADM77426 Human pla
19	45	75.0	117	9	AEBO1019 Human hea
20	45	75.0	135	9	ADM04946 PAPP-A im
21	45	75.0	256	5	ABP45589 Human Bly
22	45	75.0	256	7	ADG96416 Single ch
23	44	73.3	13	4	AAU02710 CDR regio
24	44	73.3	14	9	ADY70216 Human Mab

25	44	73.3	16	5	ABP46118 Human Bly
26	44	73.3	16	7	ADG96945 scFV VHCD
27	44	73.3	17	5	ABP46865 Human Bly
28	44	73.3	17	9	ADG97692 scFV VHCD
29	44	73.3	18	9	AEBA21444 Human ant
30	44	73.3	109	8	AD105782 Human mon
31	44	73.3	117	7	ADK18782 Anti-huma
32	44	73.3	122	4	AAU02589 Anti-edip
33	44	73.3	123	7	ADP03879 Murine-ex
34	44	73.3	123	7	ADP03878 Murine-ex
35	44	73.3	123	9	ADY70198 Human mon
36	44	73.3	127	5	ABG76565 HCV E1 an
37	44	73.3	127	7	ADK18819 Anti-huma
38	44	73.3	127	7	ADK18901 Anti-huma
39	44	73.3	127	7	ADK18607 Anti-huma
40	44	73.3	127	8	ADL25432 Human mab
41	44	73.3	127	9	AEBA21438 Human ant
42	44	73.3	129	7	ADK28407 Human ant
43	44	73.3	134	7	ADD28238 Human het
44	44	73.3	134	7	ADD28332 Human het
45	44	73.3	134	7	ADD28331 Human het

ALIGNMENTS

RESULT 1
ADR38724 standard; peptide; 11 AA.
XX ADR38724;

XX 02-DBC-2004 (first entry)
XX Mouse heavy chain variable region CDR3 seqid 126.

XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
XX toxin neutralisation; botulinum neurotoxin poisoning; mouse;
XX heavy chain variable region; complementarily determining region; CDR3.

XX Mus sp.
XX US2004175385-A1.
XX 09-SEP-2004.

XX 01-AUG-2003; 2003US-00632706.
XX 31-AUG-1998; 98US-00144886.
XX 01-AUG-2002; 2002US-0400721P.

XX (REGC) UNIV CALIFORNIA.
XX Marks JD, Amersdorfer P;
XX WPI, 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,
XX useful for diagnosing botulism or for treating pathologies associated
XX with botulinum neurotoxin poisoning.
XX Example 3; SEQ ID NO 126; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds
XX to an epitope specifically bound by an antibody expressed by a specific
XX clone where (I) binds to and neutralizes botulinum neurotoxin type A
XX (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
XX specifically bound by an antibody expressed by a clone chosen from clone
XX S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
XX 3-8, 3-10 and INGL, where (I) binds to and neutralizes botulinum
XX neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
XX comprising BoNT/A neutralising epitope having an epitope that is

CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (II) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplis. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplis, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplis. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain variable region complementarity determining
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 60; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0017;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LATYYFGLDV 11
 |||||
 1 LATYYFGLDV 11

Db 1 LATYYFGLDV 11

RESULT 2

ADR38725 standard; peptide; 11 AA.

AC ADR38725;

DT 02-DEC-2004 (first entry)

DE Mouse heavy chain variable region CDR3 seqid 127.

XX anti-bacterial; antibody; botulinum neurotoxin type A; BONT/A;

KM BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;

KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;

KM heavy chain variable region; complementarity determining region; CDR3.

OS Mus sp.

PN US2004175385-A1.

PD 09-SEP-2004.

PF 01-AUG-2003; 2003US-00632706.

PR 31-AUG-1998; 98US-00144886.

PR 01-AUG-2002; 2002US-0400721P.

PA (REGC) UNIV CALIFORNIA.

PI Marks JD, Amersdorfer P;

DR WPI; 2004-652009/63.

PT New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.

XX Example 3; SEQ ID NO 127; 110pp; English.

CC The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WRI (V), WRI (T), 3-L,

CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
 CC comprising BONT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (II) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplis. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BONT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplis, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplis. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain variable region complementarity determining
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 60; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0017;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LATYYFGLDV 11
 |||||
 1 LATYYFGLDV 11

Db 1 LATYYFGLDV 11

RESULT 3

AEB45960 standard; protein; 122 AA.

AC AEB45960;

DT 06-OCT-2005 (first entry)

DE Human monoclonal anti-MADCM antibody related protein #4.

XX Monoclonal antibody; mucosal addressin cell adhesion molecule; MADCM;

KM inflammation; inflammatory bowel disease; Crohn's disease;

KW ulcerative colitis; diverticular disease; gastritis; liver disease;

KM primary biliary cirrhosis; primary sclerosing cholangitis;

KW insulin dependent diabetes; graft versus host disease; anti-inflammatory;

KW gastrointestinal-gen.; antidiabetic; hepatotropic; antidiabetic;

OS Homo sapiens.

PN WO2005067620-A2.

PD 28-JUL-2005.

PF 07-JAN-2005; 2005WO-US000370.

PR 09-JAN-2004; 2004US-0535490P.

PA (PF12) PFIZER INC.

PA (ABGE-) ABGENIX INC.

PA (PF12) PFIZER LTD.

PI Pullen N, Molloy E, Kellermann S, Green LL, Haak-Frendschio M;

DR WPI; 2005-554958/56.

PT New antibody to Mucosal Addressin Cell Adhesion Molecule, useful for
 PT diagnosing and treating an inflammatory disease, e.g. inflammatory bowel
 PT disease, ulcerative colitis, gastritis, insulin-dependent diabetes or
 PT graft versus host disease.

PS Example 5; Fig 1; 167bp; English.

CC The invention relates to a human monoclonal antibody or its antigen-
CC binding portion that specifically binds to mucosal addressin cell
CC adhesion molecule (MacCAM). The invention also relates to a hybridoma
CC cell line that produces the human monoclonal antibody, a pharmaceutical
CC composition comprising an amount of the monoclonal antibody or its
CC antigen-binding portion and a pharmaceutical carrier, a method of
CC treating inflammatory disease in a subject, an isolated cell line that
CC produces the monoclonal antibody or its antigen-binding portion or the
CC heavy chain or light chain of the antibody or of its portion, an isolated
CC nucleic acid molecule comprising a nucleotide sequence encoding the heavy
CC chain or its antigen-binding portion or the light chain or its antigen-
CC binding portion of an antibody described above, a vector comprising the
CC nucleic acid molecule, where the vector optionally comprises an
CC expression control sequence operably linked to the nucleic acid molecule,
CC a host cell comprising the vector or the nucleic acid molecule above, a
CC method of producing a human monoclonal antibody or its antigen-binding
CC portion that specifically binds MacCAM, a method of isolating an antibody
CC or its antigen-binding portion that specifically binds to MacCAM, a
CC method of treating a subject in need of a human antibody or its antigen-
CC binding portion that specifically binds to MacCAM and inhibits binding to
CC alpha4beta7, a method of inhibiting alpha4beta7 binding to cells
CC expressing human MacCAM, a method of inhibiting MacCAM-mediated leukocyte
CC endothelial cell adhesion, migration and infiltration into tissues, a
CC method of inhibiting alpha4beta7/MacCAM-dependent cellular adhesion,
CC inhibiting the MacCAM-mediated recruitment of lymphocytes to
CC gastrointestinal lymphoid tissue, a method of diagnosing a disorder
CC characterized by circulating soluble human MacCAM and detecting
CC inflammation in a subject. The antibody, composition and methods are
CC useful for diagnosing and treating inflammatory diseases, e.g.
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC diverticular disease, gastritis, liver disease, primary biliary
CC cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and
CC graft versus host disease. This sequence represents a human monoclonal
CC anti-MacCAM antibody related protein of the invention.

SO Sequence 122 AA;

Query Match 80.0%; Score 48; DB 9; Length 122;
Best Local Similarity 63.6%; Pred. No. 2.5;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LATYYFGLDV 11
: ||||: ||
DB 100 VVTTYXXGMDV 110

RESULT 4
ADD28082
ID ADD28082 standard; protein; 114 AA.
XX
AC ADD28082;

DT 15-JAN-2004 (first entry)

DB Lymphoma related immunoglobulin variable region.

XX B-cell; malignant; immunoglobulin; immunoglobulin variable region;
KM Ig variable region; glycosylation site; lymphoma; B cell receptor;
KW cytostatic; gene therapy; glycosylation inhibitor;
XX non-Hodgkin's lymphoma.

OS Synthetic.
OS Homo sapiens.

PN WO2003074059-A2.

PD 12-SEP-2003.

PR 24-FEB-2003; 2003WO-GB000783.

XX 07-MAR-2002; 2002GB-00005395.

XX (CANC-) CANCER RES TECHNOLOGY LTD.
PA
XX Zhu D, Stevenson P;
XX WPI, 2003-902720/82.

PT Classifying a B-cell as malignant or normal by isolating a sequence
PT representing an Ig variable region from the B cell, detecting the
PT presence of a glycosylation site and classifying the cell as malignant or
PT normal.

PS Disclosure; Fig 3; 61pp; English.

CC The present invention describes a method for classifying a B-cell as
CC malignant or normal comprising: (a) isolating a sequence representing an
CC immunoglobulin (Ig) variable region from the B cell; (b) detecting the
CC presence of a glycosylation site; and (c) classifying the cell as
CC malignant or normal on the basis of the presence or absence of a
CC glycosylation site. Also described: (1) treating a patient suffering from
CC or at risk of having lymphoma; (2) screening for substances capable of
CC inhibiting glycosylation of the Ig variable region of the B cell receptor
CC; and (3) screening for substances (S) capable of inhibiting the
CC interaction between lectins of the type found in the germinal centre and
CC N-glycans found on the surface of Ig of lymphoma cells. (S) has
CC cytostatic activity, and can be used in gene therapy, and as a
CC glycosylation inhibitor. The method is useful in classifying a B-cell as
CC malignant or normal. The glycosylation inhibitor is useful in preparing a
CC medicament for treating non-Hodgkin's lymphoma. The present sequence
CC represents an Ig variable region sequence which is used in the
CC exemplification of the present invention.

SO Sequence 114 AA;

Query Match 78.3%; Score 47; DB 7; Length 114;
Best Local Similarity 77.8%; Pred. No. 3.4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFGLDV 11
: ||||: ||
DB 106 TTYXXGMDV 114

RESULT 5
ADD28323
ID ADD28323 standard; protein; 129 AA.
XX
AC ADD28323;

DT 15-JAN-2004 (first entry)

DB Human heterodimeric antibody heavy chain variable region SEQ ID NO:101.

XX human heterodimeric antibody; human; antibody; binding affinity;
KM protective antigen; Bacillus anthracis; anthrax infection; cell receptor;
KW edema factor; lethal factor; virulence; antibacterial; immunotherapy;
KM anti-toxin; anti-infective; anthrax; botulinum; smallpox;
XX Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.

OS Synthetic.
OS Homo sapiens.

PN WO2003076568-A2.

PD 18-SEP-2003.

PR 11-FEB-2003; 2003WO-US004206.

XX 11-FEB-2002; 2002US-0356086P.

PR 29-APR-2002; 2002US-0376408P.

PR 27-SEP-2002; 2002US-0414053P.

PR 25-NOV-2002; 2002US-0428807P.

PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Wild MA;
XX
DR WPI, 2003-722327/68.
XX
PT New human heterodimeric antibodies or their antibody fragments, useful as
PT anti-toxins or anti-infectives with respect to infective agents, e.g.
PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West
PT Nile virus.
XX
PS Claim 11; SEQ ID NO 101; 67pp; English.
XX
CC The present invention describes a human heterodimeric antibody (I)
CC (fragment) having a binding affinity of at least 1x10⁻⁸ M to the
CC protective antigen of Bacillus anthracis or a molecule involved in
CC anthrax infection that blocks binding of the antigen or molecule to cell
CC receptors, edema factor and lethal factor. (I) has virucide and
CC antibacterial activities, and can be used in immunotherapy. The
CC antibodies (I) are useful as anti-toxins or anti-infectives with respect
CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan
CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The
CC present sequence represents a human heterodimeric antibody heavy chain
CC variable region amino acid sequence, which is used in the exemplification
CC of the present invention.
XX
SQ Sequence 129 AA;
XX
Query Match 78.3%; Score 47; DB 7; Length 129;
Best Local Similarity 77.8%; Pred. No. 3.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
QY 3 TYYYFGLDV 11
|||:|:|
105 TYYYGMVDV 113
DB
RESULT 6
ADD28237
ID ADD28237 standard; protein; 134 AA.
XX
AC ADD28237;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:15.
XX
KW human heterodimeric antibody; human; antibody; binding affinity;
KW protective antigen; Bacillus anthracis; anthrax infection; cell receptor;
KW edema factor; lethal factor; virucide; antibacterial; immunotherapy;
KW anti-toxin; anti-infective; anthrax; botulinum; smallpox;
KW Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX MO2003076568-A2.
XX
XX PD 18-SEP-2003.
XX
XX PF 11-FEB-2003; 2003WO-US004206.
XX
XX PR 11-FEB-2002; 2002US-0356086P.
XX
XX PR 29-APR-2002; 2002US-0376408P.
XX
XX PR 27-SEP-2002; 2002US-0414053P.
XX
XX PR 25-NOV-2002; 2002US-0428807P.
XX
XX PA (ALEX-) ALEXION PHARM INC.
XX
XX PI Bowdish KS, Wild MA;
XX
XX DR WPI, 2003-722327/68.
XX

PT New human heterodimeric antibodies or their antibody fragments, useful as
PT anti-toxins or anti-infectives with respect to infective agents, e.g.
PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West
PT Nile virus.
XX
PS Claim 6; SEQ ID NO 15; 67pp; English.
XX
CC The present invention describes a human heterodimeric antibody (I)
CC (fragment) having a binding affinity of at least 1x10⁻⁸ M to the
CC protective antigen of Bacillus anthracis or a molecule involved in
CC anthrax infection that blocks binding of the antigen or molecule to cell
CC receptors, edema factor and lethal factor. (I) has virucide and
CC antibacterial activities, and can be used in immunotherapy. The
CC antibodies (I) are useful as anti-toxins or anti-infectives with respect
CC to infective agents, such as anthrax, botulinum, smallpox, Venezuelan
CC equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The
CC present sequence represents a human heterodimeric antibody heavy chain
CC variable region amino acid sequence, which is used in the exemplification
CC of the present invention.
XX
SQ Sequence 134 AA;
XX
Query Match 78.3%; Score 47; DB 7; Length 134;
Best Local Similarity 77.8%; Pred. No. 4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
QY 3 TYYYFGLDV 11
|||:|:|
DB 110 TYYYGMVDV 118
XX
RESULT 7
ADV86824
ID ADV86824 standard; protein; 134 AA.
XX
XX ADV86824;
XX
XX DT 10-MAR-2005 (first entry)
XX
DE Bacillus anthracis toxin Fab 9 K 2e G pro heavy chain variable region.
XX
XX KW Bioterrorism; Bacillus anthracis infection; vaccine; diagnosis;
XX antibacterial; antibody; heavy chain variable region.
XX
XX OS Homo sapiens.
XX
XX PN MO2004110362-A2.
XX
XX PD 23-DEC-2004.
XX
XX PF 26-MAY-2004; 2004WO-US016557.
XX
XX PR 02-JUN-2003; 2003US-00452593.
XX
XX PA (ALEX-) ALEXION PHARM INC.
XX
XX PI Bowdish KS, Frederickson S, Wild MA, Maruyama T, Nolan MJ;
XX
XX DR WPI, 2005-057715/06.
XX
XX PT Treating an animal with anthrax infection by administering an antibody to
PT the protective antigen of Bacillus anthracis, and blocking binding to
PT cell receptors, edema factor or lethal factor.
XX
XX PS Claim 7; SEQ ID NO 15; 87pp; English.
XX
CC A claimed method for treating an animal infected with Bacillus anthracis
CC comprises administering an antibody or antibody fragment that binds to a
CC molecule involved in anthrax infection and which has the ability to block
CC the binding of the molecule to at least one of a cell receptor, PA63,
CC PA63 heptamer, PA83, edema factor and lethal factor. A claimed method for
CC determining exposure to B. anthracis comprises assaying a sample for the
CC presence of a molecule selected from cell receptors, PA63, PA63 heptamer,

DR N-PSDB; ADR28116.

XX

PT Novel neuropilin binder which is scFv, antibody fragment or bioconjugate,

PT that modulates neuropilin-1 function or inhibits NP-1 dependent

PT angiogenesis of endothelial cells and/or invasion of tumor cells useful

PT for treating cancer.

XX

PS Claim 3; SEQ ID NO 29; 120bp; English.

XX

The invention relates to a neuropilin binder (NPB) (1) which is a polypeptide, antibody, scFv, antibody fragment or bioconjugate, that modulates neuropilin-1 (NP-1) function or inhibits NP-1 dependent angiogenesis of endothelial cells and/or invasion of tumour cells, whereby the NPB binds to NP-1 and modulates NP-1 function. Further disclosed is an ex vivo method of determining the dependency of the invasiveness of a naturally occurring invasive cancer cell on the functionality of NP-1. The NPB of the invention is an inhibitor of metastasis of NP-1 mediated invasion and/or adhesion and an inhibitor of tumour-associated NP-1 dependent angiogenesis. The NPB of the invention is useful for detecting NP-1 expression, modulation of NP-1 function, particularly modulation or inhibition of NP-dependent invasion or adhesion of cells, preferably tumour cells. It is useful in the manufacture of medicament for the treatment or prevention of NP-dependent angiogenesis and non-physiological blood vessel growth, particularly correlated with a tumour. It is also useful for treatment or prevention of cancer and/or metastasis of tumour cells. The current sequence

XX Sequence 244 AA; 10 36 1000047 10 8 10000344

Best Local Similarity	7
Matches	7; Conservati

Db 95 TTYYYGMDV 103

XX	AC	CCM 2005 (E. coli strain)
XX	AC	AEBA5891;
XX	AC	AEBA5891
XX	ID	AEBA5891 standard; protein; 468 AA.
AEBA5891	AEBA5891	
AEBA5891	AEBA5891	

XX
DE Human monoclonal anti-MAdCAM antibody #27.
..

KM Monoclonal antibody; mucosal addressin cell adhesion molecule; MAdCAM;
KM inflammatory bowel disease; Crohn's disease;
KM inflammation; inflammatory bowel disease

KM primary biliary cirrhosis; primary sclerosing cholangitis;
KM primary biliary cirrhosis; primary sclerosing cholangitis;
KM insulin dependent diabetes; graft versus host disease; antiinflammatory
KM gastrorotational-gen.; anticulcer; hepatotropic; antidiabetic;
KM immunosuppressive; antibody.

OS Homo sapiens.

PN WO2005067620-A2.

PD 28-JUL-2005

PF 07-JAN-2005; 2005WO-US000370.
XX

XX (PRIZ) PRIZER INC.
PA (PRIZ) PRIZER INC.

PA (PFIZ) PRIZER LTD.

XX

DR WPI; 2005-554958/56.
DR N-PSDB; AEB45890.
PT New antibody to Mucosal Adhesin Cell Adhesion Molecule, useful for
PT diagnosing and treating an inflammatory disease, e.g. inflammatory bowel
PT disease, ulcerative colitis, gastritis, insulin-dependent diabetes or
PT graft versus host disease.
XX
XX
XX Claim 8; SEQ ID NO 56; 167pp; English.
XX
XX The invention relates to a human monoclonal antibody or its antigen-
XX binding portion that specifically binds to mucosal adhesin cell
XX adhesion molecule (MadCAM). The invention also relates to a hybridoma
XX cell line that produces the human monoclonal antibody, a pharmaceutical
XX composition comprising an amount of the monoclonal antibody or its
XX antigen-binding portion and a pharmaceutical carrier, a method of
XX treating inflammatory disease in a subject, an isolated cell line that
XX produces the monoclonal antibody or its antigen-binding portion or the
XX heavy chain or light chain of the antibody or of its portion, an isolated
XX nucleic acid molecule comprising a nucleotide sequence encoding the heavy
XX chain or its antigen-binding portion or the light chain or its antigen-
XX binding portion of an antibody described above, a vector comprising the
XX nucleic acid molecule, where the vector optionally comprises an
XX expression control sequence operably linked to the nucleic acid molecule,
XX a host cell comprising the vector or the nucleic acid molecule above, a
XX method of producing a human monoclonal antibody or its antigen-binding
XX portion that specifically binds MadCAM, a method of isolating an antibody
XX or its antigen-binding portion that specifically binds to MadCAM, a
XX method of treating a subject in need of a human antibody or its antigen-
XX binding portion that specifically binds to MadCAM and inhibits binding to
XX alpha4beta7, a method of inhibiting alpha4beta7 binding to cells
XX expressing human MadCAM, a method of inhibiting MadCAM-mediated leukocyte
XX -endothelial cell adhesion, migration and infiltration into tissues, a
XX method of inhibiting alpha4beta7/MadCAM-dependent cellular adhesion,
XX inhibiting the MadCAM-mediated recruitment of lymphocytes to
XX gastrointestinal lymphoid tissue, a method of diagnosing a disorder
XX characterized by circulating soluble human MadCAM and detecting
XX inflammation in a subject. The antibody, composition and methods are
XX useful for diagnosing and treating inflammatory disease, e.g.
XX inflammatory bowel disease, Crohn's disease, ulcerative colitis,
XX diverticular disease, gastritis, liver disease, primary biliary
XX cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and
XX graft versus host disease. This sequence represents a human monoclonal
XX anti-MadCAM antibody of the invention.
SQ Sequence 468 AA;
Query Match 78.3%; Score 47; DB 9; Length 468;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 3 TYYFGLDV 11
DB 123 TYYFGMDV 131
RESURF 10
AEB45853
ID AEB45853 standard; protein; 469 AA.
XX
XX AEB45853;
AC
XX
XX 06-OCT-2005 (first entry)
DT
XX
XX Human monoclonal anti-MadCAM antibody #9.
DB Monoclonal antibody; mucosal adhesin cell adhesion molecule; MadCAM;
XX inflammation; inflammatory bowel disease; Crohn's disease;
XX ulcerative colitis; diverticular disease; gastritis; liver disease;
XX primary biliary cirrhosis; primary sclerosing cholangitis;
XX insulin dependent diabetes; graft versus host disease; antiinflammatory;
XX gastrointestinal-gen.; antidiabetic; hepatotropic; antidiabetic;
XX immunosuppressive; antibody.

XX
XX Homo sapiens.
OS
XX
XX MO2005067620-A2.
PN
XX
XX 28-JUL-2005.
PD
XX
XX 07-JAN-2005; 2005WO-US000370.
PF
XX
XX 09-JAN-2004; 2004US-0535490P.
PR
XX
XX (PFIZ) PFIZER INC.
PA (ABGE-) ABGENIX INC.
XX (PFIZ) PFIZER LTD.
XX
XX Pullen N, Molloy E, Kellermann S, Green LL, Haak-Frendescho M;
PI
XX
XX WPI; 2005-554958/56.
DR
XX
XX N-PSDB; AEB45852.
DR
XX
XX New antibody to Mucosal Adhesin Cell Adhesion Molecule, useful for
PT diagnosing and treating an inflammatory disease, e.g. inflammatory bowel
PT disease, ulcerative colitis, gastritis, insulin-dependent diabetes or
PT graft versus host disease.
XX
XX
XX Claim 8; SEQ ID NO 18; 167pp; English.
XX
XX The invention relates to a human monoclonal antibody or its antigen-
XX binding portion that specifically binds to mucosal adhesin cell
XX adhesion molecule (MadCAM). The invention also relates to a hybridoma
XX cell line that produces the human monoclonal antibody, a pharmaceutical
XX composition comprising an amount of the monoclonal antibody or its
XX antigen-binding portion and a pharmaceutical carrier, a method of
XX treating inflammatory disease in a subject, an isolated cell line that
XX produces the monoclonal antibody or its antigen-binding portion or the
XX heavy chain or light chain of the antibody or of its portion, an isolated
XX nucleic acid molecule comprising a nucleotide sequence encoding the heavy
XX chain or its antigen-binding portion or the light chain or its antigen-
XX binding portion of an antibody described above, a vector comprising the
XX nucleic acid molecule, where the vector optionally comprises an
XX expression control sequence operably linked to the nucleic acid molecule,
XX a host cell comprising the vector or the nucleic acid molecule above, a
XX method of producing a human monoclonal antibody or its antigen-binding
XX portion that specifically binds MadCAM, a method of isolating an antibody
XX or its antigen-binding portion that specifically binds to MadCAM, a
XX method of treating a subject in need of a human antibody or its antigen-
XX binding portion that specifically binds to MadCAM and inhibits binding to
XX alpha4beta7, a method of inhibiting alpha4beta7 binding to cells
XX expressing human MadCAM, a method of inhibiting MadCAM-mediated leukocyte
XX -endothelial cell adhesion, migration and infiltration into tissues, a
XX method of inhibiting alpha4beta7/MadCAM-dependent cellular adhesion,
XX inhibiting the MadCAM-mediated recruitment of lymphocytes to
XX gastrointestinal lymphoid tissue, a method of diagnosing a disorder
XX characterized by circulating soluble human MadCAM and detecting
XX inflammation in a subject. The antibody, composition and methods are
XX useful for diagnosing and treating inflammatory disease, e.g.
XX inflammatory bowel disease, Crohn's disease, ulcerative colitis,
XX diverticular disease, gastritis, liver disease, primary biliary
XX cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and
XX graft versus host disease. This sequence represents a human monoclonal
XX anti-MadCAM antibody of the invention.
SQ Sequence 469 AA;
Query Match 78.3%; Score 47; DB 9; Length 469;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 3 TYYFGLDV 11
DB 123 TYYFGMDV 131

Dd		4	ANYYYGMDV	13
	RESULT 12			
XX	ID	ADW04816	standard; peptide; 21 AA.	
XX	AC	ADW04816;		
XX	DT	07-APR-2005	(first entry)	
XX	DE	PAPP-A immunoglobulin variable domain AB b03 heavy chain CDR3 SEQ ID 141.		
XX	KM	Cytosolic; Vasotropic; heavy chain variable domain;		
XX	KN	proliferative disorder; restenosis; glioblastoma; osteosarcoma.		
XX	OS	Unidentified.		
XX	PN	US2005009136-A1.		
XX	PD	13-JAN-2005.		
XX	PF	19-FEB-2004; 2004US-00783311.		
XX	PR	19-FEB-2003; 2003US-0448515P.		
XX	PA	(DYAX-) DYAX CORP.		
XX	PI	Nixon A, Hogan S;		
XX	DR	WPI; 2005-080519/09.		
XX	PT	New pregnancy-associated plasma protein-A (PAPP-A) binding proteins		
XX	PT	comprising immunoglobulin variable domain sequences, useful for		
XX	PT	diagnosing, preventing or treating diseases such as cancer.		
XX	PS	Example; SEQ ID NO 141; 168pp; English.		
CC	CC	The present invention relates to novel proteins (I) that bind to		
CC	CC	pregnancy-associated plasma protein A (PAPP-A ADW04676). (I) comprises a		
CC	CC	first and second immunoglobulin variable domain sequence which binds to		
CC	CC	PAPP-A. Also claimed are proteins (II) which comprise light chain (Lc)		
CC	CC	and heavy chain immunoglobulin variable domain sequences which binds to		
CC	CC	PAPP-A. The proteins are useful for diagnosing, preventing or treating		
CC	CC	proliferative diseases such as glioblastoma, osteosarcoma and overgrowth		
CC	CC	of vascular smooth muscle cells following e.g., balloon angioplasty		
CC	CC	(which may cause restenosis). The proteins are especially useful for		
CC	CC	useful for treating diseases involving IGF regulated growth.The present		
CC	CC	sequence is one such immunoglobulin variable domain sequence.		
XX	XX	Sequence 21 AA;		
OY	Query Match	76.7%; Score 46; DB 9; Length 21;		
DB	Best Local Similarity	63.6%; Pred. No. 0.83; Indels 0; Gaps 0,		
	Matches	7; Conservative 2; Mismatches 2;		
		1 LATYYFGIDV 11		
		::		
		11 LGNTYYGMDV 21		
	RESULT 13			
XX	ID	ADZ41994	standard; peptide; 126 AA.	
XX	AC	ADZ41994;		
XX	DT	30-JUN-2005	(first entry)	
XX	DE	Ig H chain variable region, B-CLL set II peptide #4.		
XX	KM	Antibody; antibody engineering; antibody therapy;		
XX	KM	light chain variable region; heavy chain variable region;		

KW chronic lymphocytic leukemia; cytostatic; Hodgkins disease; lymphoma;
 KW Burkitts lymphoma; multiple myeloma; systemic lupus erythematosus;
 KW antiinflammatory; dermatological; immunosuppressive; myasthenia gravis;
 KW muscular-gen.; neuroprotective; Graves disease; antithyroid;
 KW insulin dependent diabetes; diabetes mellitus; antidiabetic;
 KW autoimmune hemolytic anemia; antianemic.
 OS Homo sapiens.
 PN WO2005034733-A2.
 XX
 XX 21-APR-2005.
 XX
 XX 08-OCT-2004; 2004WO-US033176.
 XX
 XX 08-OCT-2003; 2003US-0509473P.
 XX
 XX (NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.
 XX
 XX Messner BT, Chlorazzi N, Albesiano E;
 PI
 DR WPI; 2005-306220/31.
 XX
 PT New isolated and purified preparation of light chain and heavy chain
 PT antibody genes, useful for diagnosing, preventing or treating B cell
 PT chronic lymphocytic leukemia, or in screening for agents that may treat
 PT such disease.
 XX
 PS Disclosure; Fig 2; 58pp; English.
 XX
 XX The new invention relates to combinations of light chain antibody genes
 CC and heavy chain antibody genes, useful for treating B cell chronic
 CC lymphocytic leukemia (B-CLL). B-CLL is a disease of slowly proliferating
 CC CD5+ B lymphocytes. These cells express low levels of surface membrane Ig
 CC that serves as the receptor for antigen (BCR). Analysis of V region gene
 CC cassette usage has shown that distribution of variable region gene
 CC cassettes used by B-CLL clones differs from that in normal cells, with an
 CC increased frequency of VH3-07, VH4-34, and VH1-69 genes. This implies
 CC that the structure of the antibody molecule, and antigen specificity,
 CC play a role in the leukemic transformation of particular B cells. The
 CC present invention discloses that a significant proportion of B-CLL
 CC patients with aggressive disease share the same classes of VH, D, JH, VL
 CC and JH antibody genes, forming sets of patients with highly homologous B
 CC cell receptors. Alternatively, the patients have a disorder selected from
 CC Hodgkin's disease, non-Hodgkin's lymphoma, Burkitt's lymphoma, myeloma or
 CC systemic lupus erythematosus, myasthenia gravis, Grave's disease, type I
 CC diabetes mellitus, autoimmune peripheral neuropathy, and autoimmune
 CC hemolytic anemia. The new members of the antibody genes are: VH4-39/D6-
 CC 13/JH5/VLkappa012/2/JLkappa1/kappa2 (Set I); VH4-34/D5-
 CC 5/JH6/VLkappa012/2/JLkappa1/kappa2 (Set II); VH3-
 CC 21/JH6/VLkappa012/2/JLkappa1/kappa2 (Set III); VH1-69/D3-
 CC 16/JH3/VLkappa012/2/JLkappa1/kappa2 (Set IV); VH1-02/D6-
 CC 10/JH6/VLkappa012/2/JLkappa1/kappa2 (Set V); VH1-03/D6-
 CC 19/JH4/VLkappa012/2/JLkappa1/kappa2 (Set VI); VH1-18/D6-
 CC 19/JH4/VLkappa012/2/JLkappa1/kappa2 (Set VII); VH1-46/D6-19/JH4-
 CC 51/D6-19/JH4/VLkappa012/2/JLkappa1/kappa2 (Set VIII); VH1-69/D3-
 CC 3/JH4/VLkappa012/2/JLkappa1/kappa2 (Set IX); and VH1-69/D2-
 CC 2/JH6/VLkappa012/2/JLkappa1/kappa2 (Set X).
 CC with the above genes comprising administering an agent that binds to the
 CC antigen-binding region of an antibody encoded by the antibody genes. The
 CC agent is an anti-idiotypic antibody, a peptide antigen, or an aptamer. The
 CC present sequence is an Ig H chain variable region, B-CLL set II peptide.
 XX
 XX Sequence 126 AA:
 QY Query Match 76.7%; Score 46; DB 9; Length 126;
 DB Best Local Similarity 72.7%; Pred. No. 5.6;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 14
 ID ADW04810 standard; protein; 140 AA.
 XX
 AC ADW04810;
 XX
 DT 07-APR-2005 (first entry)
 XX
 DE PAPP-A immunoglobulin variable domain AB b03 heavy chain SEQ ID 135.
 XX
 KW Cytostatic; Vasotropic; heavy chain variable domain;
 KW proliferative disorder; restenosis; glioblastoma; osteosarcoma.
 XX
 OS Unidentified.
 XX
 PN US2005009136-A1.
 XX
 PD 13-JAN-2005.
 XX
 PF 19-FEB-2004; 2004US-00783311.
 XX
 PR 19-FEB-2003; 2003US-0448515P.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 PI Nixon A, Hogan S;
 XX
 DR WPI; 2005-080519/09.
 XX
 PT New pregnancy-associated plasma protein-A (PAPP-A) binding proteins
 PT comprising immunoglobulin variable domain sequences, useful for
 PT diagnosing, preventing or treating diseases such as cancer.
 XX
 PS Example; SEQ ID NO 135, 168pp; English.
 XX
 XX The present invention relates to novel proteins (I) that bind to
 CC pregnancy-associated plasma protein A (PAPP-A ADW04676). (I) comprises a
 CC first and second immunoglobulin variable domain sequence which binds to
 CC PAPP-A. Also claimed are proteins (II) which comprise light chain (LC)
 CC and heavy chain immunoglobulin variable domain sequences which binds to
 CC PAPP-A. The proteins are useful for diagnosing, preventing or treating
 CC proliferative diseases such as glioblastoma, osteosarcoma and overgrowth
 CC of vascular smooth muscle cells following e.g., balloon angioplasty
 CC (which may cause restenosis). The proteins are especially useful for
 CC useful for treating diseases involving IGF regulated growth. The present
 CC sequence is one such immunoglobulin variable domain sequence.
 XX
 XX Sequence 140 AA:
 QY Query Match 76.7%; Score 46; DB 9; Length 140;
 DB Best Local Similarity 63.6%; Pred. No. 6.3;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LATYYFGIDV 11
 DB 109 LGNTYYGMDV 119
 XX
 XX RESULT 15
 ID ADW04952 standard; peptide; 16 AA.
 XX
 AC ADW04952;
 XX
 DT 07-APR-2005 (first entry)
 XX
 DE PAPP-A immunoglobulin variable domain AB f03 heavy chain CDR3 SEQ ID 277.
 XX
 KW Cytostatic; Vasotropic; heavy chain variable domain;
 KW proliferative disorder; restenosis; glioblastoma; osteosarcoma.
 XX

Unidentified OS

PN US2005009136-A1.

PD 13-JAN-2005

PF 19-FEB-2004; 2004US-00783311.

PR 19-FEB-2003; 2003US-0448515P.

PA (DYAX-) DYAX CORP.

PI Nixon A, Hogan S;
xy

DR WPI; 2005-080519/09.

PT New pregnancy-associated plasma protein-A (PAPP-A) binding proteins comprising immunoglobulin variable domain sequences, useful for diagnosing, preventing or treating diseases such as cancer.

PS Example; SEQ ID NO 277; 168bp; English

The present invention relates to novel proteins (I) that bind to pregnancy-associated plasma protein A (PAPP-A, ADM04676). (I) comprises a first and second immunoglobulin variable domain sequence which binds to PAPP-A. Also claimed are proteins (II) which comprise light chain (LC) and heavy chain immunoglobulin variable domain sequences which binds to PAPP-A. The proteins are useful for diagnosing, preventing or treating proliferative diseases such as glioblastoma, osteosarcoma and overgrowth of vascular smooth muscle cells following e.g., balloon angioplasty (which may cause restenosis). The proteins are especially useful for useful for treating diseases involving IGF regulated growth. The present sequence is one such immunoglobulin variable domain sequence.

SQ Sequence 16 AA;

Query Match	75.0%	Score 45;	DB 9;	Length 16;
Best Local Similarity	63.6%	Pred NO	0.92:	

Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```
QY      1 LATYYEGLDV 11
        :| |||:|:|
Db      6 VAGYYGGMDV 16
```

Db 6 VAGYYYYGMDV 16

Search completed: December 4, 2005, 04:44:54
Job time : 98.5625 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:45 ; Search time 15.583 Seconds
(without alignments)
67.918 Million cell updates/sec

Title: US-10-632-706-127
Perfect score: 60
Sequence: 1 LATYYRGLDV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*

1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	71.7	19	2	PH1307
2	43	71.7	23	2	PH1361
3	43	71.7	29	2	PH1328
4	43	71.7	160	2	D70189
5	43	71.7	160	2	S05271
6	43	71.7	408	2	E70380
7	42	70.0	19	2	PH1304
8	42	70.0	19	2	S43960
9	42	70.0	23	2	PH1364
10	42	70.0	24	2	PT0258
11	42	70.0	27	2	PH1371
12	42	70.0	27	2	PH1355
13	42	70.0	74	2	S26793
14	42	70.0	118	2	PH1666
15	42	70.0	119	2	PH0961
16	42	70.0	120	2	PH1650
17	42	70.0	125	2	S24686
18	42	70.0	128	2	S48797
19	42	70.0	132	2	PH0954
20	42	70.0	133	2	C33548
21	42	70.0	136	2	A49047
22	42	70.0	147	2	I37780
23	42	70.0	627	2	S14683
24	40	66.7	22	2	PH1325
25	39.5	65.8	581	2	E83729
26	39	65.0	126	2	S44107
27	37	65.0	375	2	A83788
28	38	63.3	22	2	PH1359
29	38	63.3	45	2	PL0094

30	38	63.3	287	2	T27056	hypothetical prote
31	38	63.3	473	2	H86240	hypothetical prote
32	38	63.3	979	2	A39792	transcription acti
33	37	61.7	14	2	PH1601	Ig H chain V-D-J r
34	37	61.7	126	1	MHRUOU	Ig heavy chain V-I
35	37	61.7	276	2	S16892	probable transpos
36	37	61.7	447	2	T09809	NADH2 dehydrogen
37	37	61.7	448	2	T12006	glycerol-3-phospha
38	37	61.7	527	2	C70130	conditioned medium
39	37	61.7	571	2	A42138	sel-1 protein - Ca
40	37	61.7	685	2	T22223	Ig heavy chain V r
41	37	61.7	685	2	R49590	hypothetical prote
42	36.5	60.8	120	2	C75205	Ig heavy chain DJ
43	36.5	60.8	316	2	PH1368	30S ribosomal prot
44	36	60.0	18	2	PH1368	
45	36	60.0	145	2	H97707	

ALIGNMENTS

RESULT 1

PH1307
Ig heavy chain DJ region (clone C96-119) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1307
R/Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A/Reference number: PH1302; MUID:93094761; PMID:1460419
A/Accession: PH1307
A/Molecule type: DNA
A/Residues: 1-19 <WAS>
A/Cross-references: UNIPARC:UPI0000176935
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 71.7%; Score 43; DB 2; Length 19;
Best Local Similarity 66.7%; Pred. No. 0.23;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TYYRGLDV 11
DB 6 STYYRGMVDV 14

RESULT 2

PH1361
Ig heavy chain DJ region (clone C178-122B) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1361
R/Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A/Reference number: PH1302; MUID:93094761; PMID:1460419
A/Accession: PH1361
A/Molecule type: DNA
A/Residues: 1-23 <WAS>
A/Cross-references: UNIPARC:UPI0000176948
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 71.7%; Score 43; DB 2; Length 23;
Best Local Similarity 63.6%; Pred. No. 0.28;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LATYYRGLDV 11
DB 8 LFPYYRGMVDV 18

RESULT 3
PH1328
Ig heavy chain DJ region (clone C113-148) - human (fragment)
A/Residues: 1-144 <KIS2>
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1328
R/Maserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DH joining in young children with B precursor lymph
A/Reference number: PH1302; MUID:93094761; PMID:1460419
A/Accession: PH1328
A/Molecule type: DNA
A/Residues: 1-29 <MAS>
A/Cross-references: UNIPARC:UPI0000176939
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin

Query March 71.7%; Score 43; DB 2; Length 29;
Best Local Similarity 66.7%; Pred. No. 0.36;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLDV 11
: |||: |||
Db 16 STYYGMDV 24

RESULT 4
D70189
conserved hypothetical integral membrane protein B9717 - Lyme disease spirochete
C/Species: Borrelia burgdorferi (Lyme disease spirochete)
C/Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C/Accession: D70189
R/Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kierlavag, A.R.; Quackenbush, J.; Salberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A/Authors: Smith, H.O.; Venter, J.C.
A/Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A/Reference number: A70100; MUID:98055943; PMID:9403685
A/Accession: D70189
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-160 <KLB>
A/Cross-references: UNIPROT:O51659; UNIPARC:UPI0000575B2; GB:AE001171; GB:AE000783; NID
A/Experimental source: strain B31

Query March 71.7%; Score 43; DB 2; Length 160;
Best Local Similarity 60.0%; Pred. No. 2;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATYYTFFGLDV 11
: |||: |||
Db 23 ATYYTFFGLDV 32

RESULT 5
S05271
Ig heavy chain precursor - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 31-Dec-2004
C/Accession: S05271; S04602
R/Kishimoto, T.
submitted to the EMBL Data Library, March 1989
A/Reference number: S05270
A/Accession: S05271
A/Molecule type: mRNA
A/Residues: 1-160 <KIS1>
A/Cross-references: UNIPROT:Q96B9; UNIPARC:UPI0000176B50; EMBL:X14584
R/Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
A/Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of
A/Reference number: S04601; MUID:89296497; PMID:2500644
A/Accession: S04602

A/Molecule type: mRNA
A/Residues: 1-144 <KIS2>
A/Cross-references: UNIPARC:UPI0000176B51; EMBL:X14584
C/Superfamily: immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-160/Product: Ig heavy chain (fragment) #status predicted <MAT>
F/34-117/Domain: immunoglobulin homology <IMM>

Query March 71.7%; Score 43; DB 2; Length 160;
Best Local Similarity 66.7%; Pred. No. 2;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTFFGLDV 11
: |||: |||
Db 125 STYYGMDV 133

RESULT 6
E70380
Na+/H+-exchanging protein - Aquifex aeolicus
N/Alternate names: Na+/H+ antiporter
C/Species: Aquifex aeolicus
C/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C/Accession: E70380
R/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
V.
Nature 392, 353-358, 1998
A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A/Reference number: A70300; MUID:98196666; PMID:9537320
A/Accession: E70380
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-408 <AQP>
A/Cross-references: UNIPROT:O67072; UNIPARC:UPI00000564AB; GB:AE000714; NID:92983446; PIR
A/Experimental source: strain VFS
A/Genetics:
A/Gene: napa2
C/Superfamily: Aquifex aeolicus Na+/H+-exchanging protein napa1

Query March 71.7%; Score 43; DB 2; Length 408;
Best Local Similarity 54.5%; Pred. No. 5.2;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LATYYTFFGLDV 11
: |||: |||
Db 116 IVSYTFFGLDV 126

RESULT 7
PH1304
Ig heavy chain DJ region (clone C439-111) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1304
R/Maserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DH joining in young children with B precursor lymph
A/Reference number: PH1302; MUID:93094761; PMID:1460419
A/Accession: PH1304
A/Molecule type: DNA
A/Residues: 1-19 <MAS>
A/Cross-references: UNIPARC:UPI0000176934
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin

Query March 70.0%; Score 42; DB 2; Length 19;
Best Local Similarity 75.0%; Pred. No. 0.35;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYTFFGLDV 11
: |||: |||
Db 7 YYYTFFGLDV 14

RESULT 8

S43960
Ig mu chain V region (clone 18) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C:Accession: S43960
R:Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.;
Nucleic Acids Res. 22, 1389-1393, 1994
A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
A:Reference number: S43956; MUID:94248036; PMID:8190629
A:Accession: S43960
A:Molecule type: DNA
A:Residues: 1-19 <MAG>
A:Cross-references: UNIPARC:UPI000017690D
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 19;
Best Local Similarity 75.0%; Pred. No. 0.35;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
|||:|:
DB 10 YYYGMDV 17

RESULT 9

PH1364
Ig heavy chain DJ region (clone C178-136A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1364
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1364
A:Molecule type: DNA
A:Residues: 1-23 <MAS>
A:Cross-references: UNIPARC:UPI0000176949
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 23;
Best Local Similarity 75.0%; Pred. No. 0.42;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
|||:|:
DB 11 YYYGMDV 18

RESULT 10

PT0258
Ig heavy chain CDR3 region (clone 2-118B) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-May-1997
C:Accession: PT0258
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.V.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0258
A:Molecule type: DNA
A:Residues: 1-24 <YAM>
A:Cross-references: UNIPARC:UPI0000176940
A:Experimental source: B lymphocyte
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 24;

Best Local Similarity 75.0%; Pred. No. 0.44;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
|||:|:
DB 12 YYYGMDV 19

RESULT 11

PH1371
Ig heavy chain DJ region (clone C111-145) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1371
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1371
A:Molecule type: DNA
A:Residues: 1-27 <MAS>
A:Cross-references: UNIPARC:UPI000017694B
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 27;
Best Local Similarity 75.0%; Pred. No. 0.5;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
|||:|:
DB 15 YYYGMDV 22

RESULT 12

PH1355
Ig heavy chain DJ region (clone C100-136) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1355
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1355
A:Molecule type: DNA
A:Residues: 1-27 <MAS>
A:Cross-references: UNIPARC:UPI0000176945
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 27;
Best Local Similarity 75.0%; Pred. No. 0.5;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
|||:|:
DB 15 YYYGMDV 22

RESULT 13

S26793
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26793
R:Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fam
A:Reference number: S26786; MUID:92111632; PMID:1730251
A:Accession: S26793
A>Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-74 <MOR>
 A:Cross-references: UNIPARC:UPI0000115FCA; EMBL:X61019; NID:g32787; PIDN:CAA43353.1; PID
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 70.0%; Score 42; DB 2; Length 74;
 Best Local Similarity 75.0%; Pred. No. 1.4;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 YYYFGLDV 11
 |||:|:|
 Db 56 YYYGMDV 63

RESULT 14

PH1666
 Ig heavy chain V region (clone 6C9) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
 C:Accession: PH1666
 R:Hitson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
 J. Exp. Med. 178, 331-336, 1993
 A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo
 A:Reference number: PH1642; MUID:93301610; PMID:8315388
 A:Accession: PH1666
 A:Molecule type: mRNA
 A:Residues: 1-118 <HIL>
 A:Cross-references: UNIPARC:UPI0000176BE7
 A:Experimental source: B cell
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:7-30/Domain: immunoglobulin homology <IMM>

Query Match 70.0%; Score 42; DB 2; Length 118;
 Best Local Similarity 75.0%; Pred. No. 2.2;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 YYYFGLDV 11
 |||:|:|
 Db 100 YYYGMDV 107

RESULT 15

PH0961
 Ig heavy chain V region (G6+ T-133) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
 C:Accession: PH0961
 R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A:Title: Evidence for somatic selection of natural autoantibodies.
 A:Reference number: PH0952; MUID:92202860; PMID:1552291
 A:Accession: PH0961
 A>Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-119 <MAR>
 A:Cross-references: UNIPARC:UPI0000176CE5
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-50/Region: framework 2
 F:51-67/Region: complementarity-determining 2
 F:68-98/Region: framework 3
 F:99-107/Region: complementarity-determining 3

Query Match 70.0%; Score 42; DB 2; Length 119;
 Best Local Similarity 75.0%; Pred. No. 2.2;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 YYYFGLDV 11
 |||:|:|

Db 101 YYYGMDV 108

Search completed: December 4, 2005, 04:53:32
 Job time : 17.583 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:36 ; Search time 100.375 Seconds
(without alignments)
77.318 Million cell updates/sec

Title: US-10-632-706-127
Perfect score: 60
Sequence: 1 LATYYFGLDV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80: *
1: uniprot_sprot: *
2: uniprot_crembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	44	73.3	1348	2	Q4N9V2_THBPA	Q4N9V2 thelteria p
2	44	73.3	2262	2	Q4U9Y8_THBPA	Q4U9Y8 thelteria a
3	43	71.7	160	2	O51659_BORBU	O51659 borrelia bu
4	43	71.7	160	2	O660F6_BORGA	O660F6 borrelia ga
5	43	71.7	408	2	O67072_AOUAE	O67072 aquifex aeo
6	42	70.0	364	2	O7VY71_BORBP	O7VY71 borrelia
7	42	70.0	364	2	O7W926_BORBP	O7W926 borrelia
8	42	70.0	364	2	O7W926_BORBP	O7W926 borrelia
9	42	70.0	378	2	O4QAI0_LEIMA	O4QAI0 leishmania
10	42	70.0	382	2	O89NT9_BRAJA	O89NT9 bradyrhizob
11	42	70.0	594	2	O74N07_NAMEO	O74N07 nanoarchaeu
12	42	70.0	606	2	O6GMV2_HUMAN	O6GMV2 homo sapien
13	42	70.0	1062	2	O96X97_SUITO	O96X97 sulfobacil
14	42	70.0	3212	2	O4FWX4_LEIMA	O4FWX4 leishmania
15	41	68.3	716	2	O6A021_DESPS	O6A021 desulfohalo
16	40	66.7	288	2	O6F6N6_ACIAD	O6F6N6 acinetobact
17	40	66.7	291	2	O4ZUB1_PBSBY	O4ZUB1 pseudomonas
18	40	66.7	293	2	O6D023_ERWCT	O6D023 erwina car
19	40	66.7	447	2	O8BU78_OCRTH	O8BU78 oceanobacil
20	40	66.7	702	2	O8C3X8_MOUSE	O8C3X8 mus musculu
21	40	66.7	978	2	O5AAV6_CANAL	O5AAV6 candida alb
22	40	66.7	1113	2	O6WE05_ARALY	O6WE05 arabidopsis
23	40	66.7	3964	2	O4OBV4_LEIMA	O4OBV4 leishmania
24	39.5	65.8	581	1	Y637_BRCHD	O9Kf49 bacillus ha
25	39	65.0	188	2	O5ZG31_MAGGR	O5ZG31 magnaporthe
26	39	65.0	215	2	O5IXQ2_NOCPA	O5IXQ2 nocardia fa
27	39	65.0	317	2	O97BK3_THERVO	O97BK3 thermoplaem
28	39	65.0	375	2	O9KDV6_BACDH	O9KDV6 bacillus ha
29	39	65.0	419	2	O82700_MEDTR	O82700 medicago tr
30	39	65.0	423	2	O9S7A5_MEDTR	O9S7A5 medicago tr
31	39	65.0	434	2	O6ZBX7_ORISA	O6ZBX7 oryza sativ

32	39	65.0	451	2	O6ZBX6_ORISA	O6ZBX6 oryza sativ
33	39	65.0	478	2	O6PIB1_HUMAN	O6PIB1 homo sapien
34	39	65.0	662	2	O8BRT5_LACPL	O8BRT5 lactobacill
35	39	65.0	701	1	LSP2_DROME	O24388 drosophila
36	39	65.0	779	2	O6S5Z1_MANSW	O6S5Z1 mannaetima
37	39	65.0	780	2	O7V0H6_CANBF	O7V0H6 candidatus
38	38	63.3	116	2	O7Z3Y6_HUMAN	O7Z3Y6 homo sapien
39	38	63.3	148	2	O5TMX6_HUMAN	O5TMX6 anopheles g
40	38	63.3	159	2	O96QSO_HUMAN	O96QSO homo sapien
41	38	63.3	239	2	O5X0G3_LEGPL	O5X0G3 legioneila
42	38	63.3	243	2	O5Z2F4_LEGPH	O5Z2F4 legioneila
43	38	63.3	307	2	O6N5D3_RHOPA	O6N5D3 rhodospseudo
44	38	63.3	350	2	O8CVT5_METKA	O8CVT5 methanopyru
45	38	63.3	366	2	O9XTT1_CAEEL	O9XTT1 caenorhabdi

ALIGNMENTS

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RESULT 1
Q4N9V2_THBPA PRELIMINARY; PRT; 1348 AA.
ID Q4N9V2;
AC Q4N9V2;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=TP01_0021;
OS Thelteria parva.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
OX NCBI_Taxid=5875;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muga;
RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
RA Hall N., Ren O., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,
RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
RA Jiang L., Lynn J., Weaver B., Shoabli A., Masawo D., Crabtree J.,
RA Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C., Suh B.,
RA Silva J.C., Utecherback T.R., Feldblyum T.V., Pertea M., Allen J.,
RA Taracha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,
RA Venter J.C., Frazer C.M., Nene V.;
RA "Genome sequence of Theileria parva, a bovine pathogen that transforms
RT lymphocytes.";
RL Science 309:134-137(2005).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Muga;
RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA Ren O., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
RA Lynn J., Weaver B., Shoabli A., Masawo D., Crabtree J., Wortman J.R.,
RA Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA Utecherback T., Feldblyum T., Pertea M., Allen J., Taracha E.L.,
RA Salzberg S.L., Nene V.;
RA Frazer C.M., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAKG0100001; EAKJ3265.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 1348 AA; 155635 MW; 474C3A40C23E8C5F CRC64;

Query Match 73.3%; Score 44; DB 2; Length 1348;
Best Local Similarity 87.5%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
Q4UFY8 THEAN PRELIMINARY; PRT; 2262 AA.
ID Q4UFY8 THEAN PRELIMINARY; PRT; 2262 AA.
AC Q4UFY8 THEAN PRELIMINARY; PRT; 2262 AA.
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=TA19710;
OS Theileria annulata.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
OC Theileria.
NCBI_TaxID=5874;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ankara isolate clone C9;
RA Pain A., Renaud H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
RA Hall N., Barrett B.G.;
RT "The chromosome 1 sequence of Theileria annulata."
RL Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: CR940347; CA174001.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ
SEQUENCE 2262 AA; 262068 MW; FD9E8915243EF512 CRC64;

Query Match
Best Local Similarity 73.3%; Score 44; DB 2; Length 2262;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTYFFGLD 10
Db 1244 SYFFGLD 1251

RESULT 3
Q51659 BORBU PRELIMINARY; PRT; 160 AA.
ID Q51659 BORBU PRELIMINARY; PRT; 160 AA.
AC Q51659;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Conserved hypothetical integral membrane protein.
GN OrderedLocustNames=B80717;
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
OC Borrelia burgdorferi group.
NCBI_TaxID=139;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 35210 / B31;
RL MEDLINE=98065943; PubMed=9403685; DOI=10.1038/37551;
RA Fraser C.M., Castens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R.J., Hickey B.K.,
RA Gwinn M.L., Dougherty B.A., Tomb J.-F., Fleischmann R.D.,
RA Richardson D.L., Peterson J.D., Karlson A.R., Quackenbush J.,
RA Salzberg S.L., Hanson M., Van Vugt R., Palmer N., Adams M.D.,
RA Gocayne J.D., Weidman J.F., Uterback T.R., Matthey L., McDonald L.A.,
RA Artach P., Bowman C., Garland S.A., Fujii C., Cotton M.D., Horek K.,
RA Roberts K.W., Hatch B., Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochete, Borrelia
burgdorferi."
RL Nature 390:580-586(1997).
DR EMBL: AE001171; AAC67057.1; -; Genomic_DNA.
DR PIR: D70189; D70189.
KW Complete proteome; Hypothetical protein.
SQ
SEQUENCE 160 AA; 19300 MW; 9DE28A497C0F5737 CRC64;

Query Match
Best Local Similarity 71.7%; Score 43; DB 2; Length 160;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATYYFGLDV 11
Db 23 ATYYFSDI 32
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Db 23 ATYYFSDI 32

RESULT 4
Q660F6 BORGA PRELIMINARY; PRT; 160 AA.
ID Q660F6 BORGA PRELIMINARY; PRT; 160 AA.
AC Q660F6;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Conserved hypothetical integral membrane protein.
GN OrderedLocustNames=BG0739;
OS Borrelia garinii.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
OC Borrelia burgdorferi group.
NCBI_TaxID=29519;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PB1;
RA Gloeckner G., Lehmann R., Romwaldt A., Pradella S.,
RA Schulte-Spechtel U., Wilske B., Snel J., Platzner M.;
RT "Comparative analysis of the Borrelia garinii genome."
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: CP000013; AAU07565.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ
SEQUENCE 160 AA; 19293 MW; B5B15C5197BFB89 CRC64;

Query Match
Best Local Similarity 71.7%; Score 43; DB 2; Length 160;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATYYFGLDV 11
Db 23 ATYYFSDI 32

RESULT 5
Q67072 AQUAE PRELIMINARY; PRT; 408 AA.
ID Q67072 AQUAE PRELIMINARY; PRT; 408 AA.
AC Q67072;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Na(+)/H(+) antiporter.
GN Name=napA2; OrderedLocustNames=AQ_929;
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OC NCBI_TaxID=63363;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VF5;
RL MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
RA Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Kallier M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olsen G.J., Sanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
aeolicus."
RL Nature 392:353-358(1998).
DR EMBL: AE000714; AAC07034.1; -; Genomic_DNA.
DR PIR: E70380; E70380.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO: GO:0006885; P:regulation of pH; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR006153; Na_H_porter.
DR Pfam: PF00999; Na_H_Exchange; 1.
KW Complete proteome; Transmembrane; Transport.
SQ
SEQUENCE 408 AA; 43582 MW; 7E05B4B387A6C506 CRC64;

Query Match
Best Local Similarity 71.7%; Score 43; DB 2; Length 408;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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QY 1 LATYYPFGADV 11
    : : : : :
Db 116 IVSYYPFGDL 126

RESULT 6
Q7VY71 BORPE PRELIMINARY; PRT; 364 AA.
ID Q7VY71 BORPE PRELIMINARY; PRT; 364 AA.
AC Q7VY71;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative periplasmic solute-binding protein.
GN Name=smom; OrderedLocNames=Bp1487;
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxId=520;
KW [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebathia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640415; CAB31776.1; -; Genomic_DNA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006311; Tat.
DR InterPro; IPR004682; TRAP_transpDctP.
DR Pfam; PF03480; SBP_bac_7_1.
DR TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
KW Complete proteome.
SQ SEQUENCE 364 AA; 40021 MW; 03F1C2B6FC51D502 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 364;
Best Local Similarity 77.8%; Pred. No. 38;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATYYFGDL 10
    : : : : :
Db 98 ASYYFGKD 106

RESULT 7
Q7W926 BORPA PRELIMINARY; PRT; 364 AA.
ID Q7W926 BORPA PRELIMINARY; PRT; 364 AA.
AC Q7W926;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative periplasmic solute-binding protein.
GN Name=smom; OrderedLocNames=Bp1948;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxId=519;
KW [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebathia M., Preston A., Murphy L.D., Thomson N.R.,
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RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640428; CAB37248.1; -; Genomic DNA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006311; Tat.
DR InterPro; IPR004682; TRAP_transpDctP.
DR Pfam; PF03480; SBP_bac_7_1.
DR TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
KW Complete proteome.
SQ SEQUENCE 364 AA; 39967 MW; 9700BC4608CFID8 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 364;
Best Local Similarity 77.8%; Pred. No. 38;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATYYFGDL 10
    : : : : :
Db 98 ASYYFGKD 106

RESULT 8
Q7WKH1 BORBR PRELIMINARY; PRT; 364 AA.
ID Q7WKH1 BORBR PRELIMINARY; PRT; 364 AA.
AC Q7WKH1;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Putative periplasmic solute-binding protein.
GN Name=smom; OrderedLocNames=BB2116;
OS Bordetella bronchiseptica (Alcaligenes bronchiseptica).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxId=518;
KW [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebathia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Felwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640443; CAB32632.1; -; Genomic_DNA.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006311; Tat.
DR InterPro; IPR004682; TRAP_transpDctP.
DR Pfam; PF03480; SBP_bac_7_1.
DR TIGRFAMs; TIGR01409; TAT_signal_seq; 1.
KW Complete proteome.
SQ SEQUENCE 364 AA; 39997 MW; 8AB672BA3BF09AD CRC64;

Query Match 70.0%; Score 42; DB 2; Length 364;
Best Local Similarity 77.8%; Pred. No. 38;
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Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 2 ATYYFGLD 10
|:|||||
Db 98 ASYYFGKD 106

RESULT 9

Q40A10 LEIMA

ID Q40A10 LEIMA PRELIMINARY; PRT; 378 AA.

AC Q40A10; 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DE Hypothetical protein.
GN ORFNames=LmjF25.0840;
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxId=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RA Peacock C.S.; Murphy L.; Ivens A.C.; Berriman M.; Blackwell J.;
RA Smith D.; Collins M.; Foster N.; Harris D.; Oliver K.; O'Neill S.;
RA Saunders D.; Seeger K.; Warren T.; Rajandream M.; and Barrell B.G.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CTO05264; CAJ04989.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 378 AA; 41605 MW; 9E3BE7C7C1F04839 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 378;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TYYFGL 9
|:|||||
Db 112 TYYFGL 118

RESULT 10

Q89NT9 BRAJA

ID Q89NT9 BRAJA PRELIMINARY; PRT; 382 AA.

AC Q89NT9; 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DE Periplasmic mannitol-binding protein.
GN OrderedLocustNames=blj3745;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxId=375;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=USDA 110;
RA MEDLIN=2248498; PubMed=12597275;
RA Kaneko T.; Nakamura Y.; Sato S.; Minamisawa K.; Uchiyama T.;
RA Saeemoo S.; Matsumoto M.; Shimo S.; Tsunoka H.; Wada T.; Yamada M.;
RA Kohara M.; Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.",
RL DNA Res. 9:189-197 (2002).

DR EMBL; BA000040; BAC49010.1; -; Genomic_DNA.
DR GO; GO:0003288; C:periplasmic space (sensu Gram-negative Bact. .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006311; Tac.
DR InterPro; IPR004682; TRAP transpDctP.
DR Pfam; PF03480; SBP_bac_7_1.
DR TIGRFAMs; TIGR01405; TAT_signal_seq; 1.
KW Complete proteome.
SQ SEQUENCE 382 AA; 42090 MW; 23C26498A9F9B8D CRC64;

Query Match 70.0%; Score 42; DB 2; Length 382;
Best Local Similarity 77.8%; Pred. No. 40;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATYYFGLD 10
|:|||||
Db 117 ASYYFGKD 125

RESULT 11

Q7AN07 NANOQ

ID Q7AN07 NANOQ PRELIMINARY; PRT; 594 AA.

AC Q7AN07; 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE NEQ353.
GN OrderedLocustNames=NEQ353;
OS Nanoarchaeum equitans.
OC Archaea; Nanoarchaeota; Nanoarchaeum.
OX NCBI_TaxId=160232;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Kin4-M;
RX PubMed=1456062; DOI=10.1073/pnas.1735403100;
RA Waters E.; Hohn M.J.; Abel I.; Graham D.E.; Adams M.D.; Barnstead M.;
RA Beeson K.Y.; Bibbs L.; Bolanos R.; Keller M.; Kretz K.; Lin X.;
RA Mathur E.; Ni J.; Podar M.; Richardson T.; Sutton G.G.; Simon M.;
RA Soell D.; Stetter K.O.; Short J.M.; Noordwyler M.;
RT "The genome of Nanoarchaeum equitans: insights into early archaeal
RT evolution and derived parasitism."
RL Proc. Natl. Acad. Sci. U.S.A. 100:12984-12988 (2003).
DR EMBL; AB017199; AAR39202.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 594 AA; 69673 MW; FD2E60ACF00CD9F4 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 594;
Best Local Similarity 54.5%; Pred. No. 62;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LATYYFGLDV 11
|:|||||
Db 569 LSRYYFGVDI 579

RESULT 12

Q6GMV2 HUMAN

ID Q6GMV2 HUMAN PRELIMINARY; PRT; 606 AA.

AC Q6GMV2; 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE IGHM protein.
GN Name=IGHM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLIN=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;

DR Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
DR Klausner R.D.; Collins F.S.; Wagner L.; Shennan C.M.; Schuler G.D.;
DR Altchul S.F.; Zeeberg B.; Buetow K.H.; Scheffer C.F.; Bhat N.K.;
DR Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
DR Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
DR Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
DR Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carrinci P.; Prange C.;
DR Raha S.C.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullany S.J.;
DR Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;
DR Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Huiyk S.W.;


```
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallue D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073758; AAH73758.1; -; mRNA.
DR SMR; O6GM2; 20-256.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 606 AA; 66185 MW; B6B38B5114E4C55 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 606;
Best Local Similarity 75.0%; Pred. No. 63;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Cy 4 YYYEGLDV 11
Db 135 YYYGMDV 142

RESULT 13
O96X97.SULTO PRELIMINARY; PRT; 1062 AA.
ID O6X97.SULTO
AC O96X97;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1062aa long hypothetical thermopspn.
GN OrderedLocustNames=ST72615;
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=11955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=JCM 10545 / ?;
RG MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankaï H., Kobayashi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7."
RL DNA Res. 8:123-140(2001).
DR EMBL; BA000023; BAB67731.1; -; Genomic_DNA.
DR InterPro; IPR007981; Peptidase_A5.
DR Pfam; PF05317; Thermopspn; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1062 AA; 118024 MW; 166FAED60A040DB4 CRC64;

Query Match 70.0%; Score 42; DB 2; Length 1062;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 3 TYYEGL 9
Db 623 TYYEGL 629

RESULT 14
O4FWX4.LEIMA
ID O4FWX4.LEIMA PRELIMINARY; PRT; 3212 AA.
AC O4FWX4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=LMU_1075;
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RX PubMed=16020728; DOI=10.1126/science.1112660;
RA Ivens A.C., Peacock C.S., Worthey E.A., Murphy L., Aggarwal G.,
RA Berriman M., Siak E., Rajandream M.A., Adlem E., Aert R., Anupama A.,
RA Apostolou Z., Attipoe P., Baeson N., Bauser C., Beck A., Beverley S.M.,
RA Biscuettin G., Borzym K., Bothe G., Brusch C.V., Collins M.,
RA Cadag E., Clarion L., Clayton C., Coulson R.M., Cronin A., Cruz A.K.,
RA Davies R.M., De Gaudenzi J., Dobson D.E., Duesterhoelt A.,
RA Fazelina G., Foster N., Frasch A.C., Fraser A., Fuchs M., Gabel C.,
RA Goble A., Goffeau A., Harris D., Hertz-Fowler C., Hilbert H., Horn D.,
RA Huang Y., Klages S., Knights A., Kube M., Larke N., Livyn L.,
RA Lord A., Louie T., Marra M., Masuy D., Matthews K., Michael S.,
RA Mottarm J.C., Muller-Auer S., Munden H., Nelson S., Norbertczak H.,
RA Oliver K., O'Neill S., Pentony M., Pohl T.M., Price C., Purnelle B.,
RA Quail M.A., Rabinowitch E., Reinhardt R., Rieger M., Rinta J.,
RA Robben J., Robertson L., Ruiz J.C., Rutter S., Saunders D.,
RA Schaefer M., Schein J., Schwartz D.C., Seeger K., Seyler A., Sharp S.,
RA Shin H., Sivam D., Squares R., Squares S., Toledo V., Vogt C.,
RA Voickaert G., Wambut H., Warren T., Wedler H., Woodward J., Zhou S.,
RA Zimmermann W., Smith D.F., Blackwell J.M., Stuart K.D., Barrell B.,
RA Myler P.J.;
RT "The genome of the Kinetoplastid Parasite, Leishmania major."
RL Science 309:436-442(2005).
DR EMBL; CP000081; AA214369.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 3212 AA; 342958 MW; E26EA125060F8A6B CRC64;

Query Match 70.0%; Score 42; DB 2; Length 3212;
Best Local Similarity 70.0%; Pred. No. 3.3e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 1 LATYYFGLD 10
Db 164 LAGYYFGVE 173

RESULT 15
O6AQZ1.DESPS
ID O6AQZ1.DESPS PRELIMINARY; PRT; 716 AA.
AC O6AQZ1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Related to mercuric reductase.
GN OrderedLocustNames=DP0504;
OS Desulfotalea psychrophila.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
OC Desulfobulbaceae; Desulfotalea.
OX NCBI_TaxID=84980;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=LSv54 / DSM 12343;
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RX PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;
 RA Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
 RA Bauer M., Zibat A., Lombardot T., Becker I., Amann U., Gellner K.,
 RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
 RA Klenk H.-P.;
 RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
 RT from permanently cold Arctic sediments.";
 RL Environ. Microbiol. 6:887-902(2004).
 DR EMBL: CR522870; CAC35233.1; -; Genomic DNA.
 DR GO: GO:0005277; C:cytoplasm; IEA.
 DR GO: GO:0015036; F:disulfide oxidoreductase activity; IEA.
 DR GO: GO:0050660; F:FAD binding; IEA.
 DR GO: GO:0006118; P:electron transport; IEA.
 DR InterPro: IPR001327; FAD_pyr_redox.
 DR InterPro: IPR000815; Hg_reductase.
 DR InterPro: IPR006162; Ppancne S.
 DR InterPro: IPR001100; Pyr_redox.
 DR InterPro: IPR004099; Pyr_redox_dim.
 DR Pfam: PF00070; Pyr_redox; 2.
 DR Pfam: PF02852; Pyr_redox_dim; 1.
 DR PRINTS: PR00368; FADPNR.
 DR PRINTS: PR00945; HGRDTRSE.
 DR PRINTS: PR00411; PNDRTRASE.
 DR PRODOM: PD000139; FAD_pyr_redox; 1.
 DR PROSITE: PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
 DR PROSITE: PS00076; PYRIDINE_REDOX_1; 1.
 KM Complete proteome.
 SQ SEQUENCE 716 AA; 78725 MW; 68EFC0600DE44094 CRC64;

Query Match 68.3%; Score 41; DB 2; Length 716;
 Best Local Similarity 60.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 LATYVFGLD 10
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 Db 14 VSAIYFGLD 23

Search completed: December 4, 2005, 04:52:20
 Job time : 104.375 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 03:59:51 : Search time 23.6042 Seconds
(without alignments)
38.528 Million cell updates/sec

Title: US-10-632-706-127

Perfect score: 60

Sequence: 1 LATYYFGIDV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/prodata/1/aa/6 COMB.pep:*
- 3: /cgn2_6/prodata/1/aa/H COMB.pep:*
- 4: /cgn2_6/prodata/1/aa/PCTUS COMB.pep:*
- 5: /cgn2_6/prodata/1/aa/RE COMB.pep:*
- 6: /cgn2_6/prodata/1/aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	43	71.7	33	1	US-08-053-131-78
2	43	71.7	33	1	US-08-645-641-78
3	43	71.7	33	1	US-07-853-408B-78
4	43	71.7	33	1	US-08-096-762-78
5	43	71.7	33	1	US-08-308-865-78
6	43	71.7	33	2	US-09-042-353-275
7	43	71.7	33	2	US-08-758-417A-123
8	43	71.7	33	4	PCT-US92-10983-78
9	43	71.7	125	2	US-08-840-459-84
10	43	71.7	125	2	US-09-497-625A-84
11	42	70.0	29	1	US-08-053-131-73
12	42	70.0	29	1	US-08-645-641-73
13	42	70.0	29	1	US-07-853-408B-73
14	42	70.0	29	1	US-08-096-762-73
15	42	70.0	29	1	US-08-308-865-73
16	42	70.0	29	2	US-09-042-353-270
17	42	70.0	29	2	US-08-758-417A-118
18	42	70.0	29	4	PCT-US92-10983-73
19	42	70.0	31	1	US-08-053-131-83
20	42	70.0	31	1	US-08-645-641-83
21	42	70.0	31	1	US-07-853-408B-83
22	42	70.0	31	1	US-08-096-762-83
23	42	70.0	31	1	US-08-308-865-83
24	42	70.0	31	2	US-09-042-353-280
25	42	70.0	31	2	US-08-758-417A-128
26	42	70.0	31	4	PCT-US92-10983-83
27	42	70.0	36	1	US-08-053-131-84

28	42	70.0	36	1	US-08-645-641-84	Sequence 84, App1
29	42	70.0	36	1	US-07-853-408B-84	Sequence 84, App1
30	42	70.0	36	1	US-08-096-762-84	Sequence 84, App1
31	42	70.0	36	1	US-08-308-865-84	Sequence 84, App1
32	42	70.0	36	2	US-09-042-353-281	Sequence 281, App
33	42	70.0	36	2	US-08-758-417A-129	Sequence 84, App1
34	42	70.0	36	4	PCT-US92-10983-84	Sequence 84, App1
35	42	70.0	119	2	US-08-840-459-88	Sequence 88, App1
36	42	70.0	119	2	US-09-497-625A-88	Sequence 88, App1
37	42	70.0	128	2	US-09-840-459-77	Sequence 77, App1
38	42	70.0	128	2	US-09-840-459-79	Sequence 79, App1
39	42	70.0	128	2	US-09-497-625A-77	Sequence 79, App1
40	42	70.0	128	2	US-09-497-625A-79	Sequence 80, App1
41	42	70.0	167	2	US-09-472-087-80	Sequence 80, App1
42	42	70.0	236	2	US-09-456-090A-64	Sequence 64, App1
43	42	70.0	236	2	US-09-456-090A-104	Sequence 104, App
44	42	70.0	236	2	US-09-453-234-64	Sequence 64, App1
45	42	70.0	236	2	US-09-453-234-104	Sequence 104, App

ALIGNMENTS

RESULT 1
US-08-053-131-78
Sequence 78, Application US/08053131
Patent No. 5661016
GENERAL INFORMATION:
APPLICANT: Londey, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Klourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 200
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,131
FILING DATE: 26-APR-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14633-9-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-053-131-78

Query Match 71.7%; Score 43; DB 1; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTGLDV 11
:||||:|
DB 10 SYTYGMDV 18

RESULT 2

US-08-645-641-78
; Sequence 78, Application US/08645641
; Patent No. 5719032
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,641
; FILING DATE: 20-MAY-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/904,068
; FILING DATE: 23-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-000913
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-645-641-78

Query Match 71.7%; Score 43; DB 1; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTGLDV 11
:||||:|
DB 10 SYTYGMDV 18

RESULT 3

US-07-853-408B-78
; Sequence 78, Application US/07853408B
; Patent No. 5789650
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies

; NUMBER OF SEQUENCES: 150
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/853,408B
; FILING DATE: 19920318

; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14643-9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-853-408B-78

Query Match 71.7%; Score 43; DB 1; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYTGLDV 11
:||||:|
DB 10 SYTYGMDV 18

RESULT 4

US-08-096-762-78
; Sequence 78, Application US/08096762
; Patent No. 5814318
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 200
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,762
; FILING DATE: 22-JUL-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,860

FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-4
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-096-762-78

Query Match 71.7%; Score 43; DB 1; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYRFGLDV 11
:||||:|
DB 10 SYYYGMDV 18

RESULT 5
US-08-308-865-78
Sequence 78, Application US/08308865
Patent No. 5877397
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSER: William M. Smith
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,865
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/145,707
FILING DATE:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-308-865-78

Query Match 71.7%; Score 43; DB 1; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYRFGLDV 11
:||||:|
DB 10 SYYYGMDV 18

RESULT 6
US-09-042-353-275
Sequence 275, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741

FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 275:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-042-353-275

Query Match 71.7% Score 43; DB 2; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYRGLDV 11
:||||:|
DB 10 SYTYGMDV 18

RESULT 7
US-08-758-417A-123
Sequence 123, Application US/08758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-DEC-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996

APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Serfati, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 123:
US-08-758-417A-123

Query Match 71.7% Score 43; DB 2; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYRGLDV 11
:||||:|
DB 10 SYTYGMDV 18

RESULT 8
PCT-US92-10983-78
Sequence 78, Application PC/TUS9210983
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 152
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10983
FILING DATE: 19921217
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-2

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US92-10983-78

Query Match      71.7%; Score 43; DB 4; Length 33;
Best Local Similarity 66.7%; Pred. No. 1.6;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 TTYFGLDV 11
      :|||:|:|
Db      10 SYTYGMDV 18

RESULT 9
US-09-840-459-84
Sequence 84, Application US/09840459
Patent No. 6696350
GENERAL INFORMATION:
APPLICANT: Larosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 84
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
US-09-840-459-84

Query Match      71.7%; Score 43; DB 2; Length 125;
Best Local Similarity 66.7%; Pred. No. 6.4;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 TTYFGLDV 11
      :|||:|:|
Db      106 SYTYGMDV 114

RESULT 10
US-09-497-625A-84
Sequence 84, Application US/09497625A
Patent No. 6727349
GENERAL INFORMATION:
APPLICANT: Larosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
```

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TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
FILE REFERENCE: 1855.1052-004
CURRENT APPLICATION NUMBER: US/09/497,625A
CURRENT FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 106
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 84
LENGTH: 125
TYPE: PRT
ORGANISM: Homo sapiens
US-09-497-625A-84

Query Match      71.7%; Score 43; DB 2; Length 125;
Best Local Similarity 66.7%; Pred. No. 6.4;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 TTYFGLDV 11
      :|||:|:|
Db      106 SYTYGMDV 114

RESULT 11
US-08-053-131-73
Sequence 73, Application US/08053131
Patent No. 5661016
GENERAL INFORMATION:
APPLICANT: Lomborg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
FILE REFERENCE: 197
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Tower, Suite 200
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,131
FILING DATE: 26-APR-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
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TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-053-131-73

Query Match 70.0%; Score 42; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 2.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
|||:|:|
DB 7 YYYGMDV 14

RESULT 12
US-08-645-641-73
Sequence 73, Application US/08645641
Patent No. 5719032
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
ATTORNEY/AGENT INFORMATION:
NAME: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5719032-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/645,641
FILING DATE: 20-May-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-000913
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-645-641-73

Query Match 70.0%; Score 42; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 2.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
|||:|:|
DB 7 YYYGMDV 14

RESULT 13
US-07-853-408B-73
Sequence 73, Application US/07853408B
Patent No. 5789650
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils

APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Stuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/853,408B
FILING DATE: 19920318
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-853-408B-73

Query Match 70.0%; Score 42; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 2.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
|||:|:|
DB 7 YYYGMDV 14

RESULT 14
US-08-096-762-73
Sequence 73, Application US/08096762
Patent No. 5814318
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
ATTORNEY/AGENT INFORMATION:
NAME: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5814318-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 210
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stuart Tower, Suite 200
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,762
FILING DATE: 22-JUL-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131

FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-4
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-096-762-73

Query Match 70.0%; Score 42; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 2.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
|||:|:
DB 7 YYYGMDV 14

RESULT 15
US-08-308-865-73
Sequence 73, Application US/0830865
Patent No. 5877397
GENERAL INFORMATION:
APPLICANT: Londerg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5877397-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/308,865
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/145,707
FILING DATE:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-1-1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-308-865-73

Query Match 70.0%; Score 42; DB 1; Length 29;
Best Local Similarity 75.0%; Pred. No. 2.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YYYFGLDV 11
|||:|:
DB 7 YYYGMDV 14

Search completed: December 4, 2005, 04:09:43
Job time: 24.6042 secs

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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:07:28 ; Search time 78.8333 Seconds
(without alignments)
58.302 Million cell updates/sec

Title: US-10-632-706-127
Perfect score: 60
Sequence: 1 LATYYFGLDV 11

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	11	4	US-10-632-706-126 Sequence 126, App
2	60	100.0	11	4	US-10-632-706-127 Sequence 127, App
3	48	80.0	122	6	US-11-031-485-116 Sequence 116, App
4	47	78.3	129	4	US-10-364-743-101 Sequence 101, App
5	47	78.3	129	5	US-10-452-593-101 Sequence 101, App
6	47	78.3	134	4	US-10-364-743-101 Sequence 15, App
7	47	78.3	134	5	US-10-452-593-101 Sequence 15, App
8	47	78.3	134	5	US-11-031-485-116 Sequence 56, App
9	47	78.3	134	5	US-11-031-485-116 Sequence 18, App
10	46	76.7	13	4	US-10-632-706-114 Sequence 114, App
11	46	76.7	21	5	US-10-783-311-141 Sequence 141, App
12	46	76.7	140	5	US-10-783-311-135 Sequence 135, App
13	45	75.0	16	5	US-10-783-311-277 Sequence 277, App
14	45	75.0	21	3	US-09-880-748-3068 Sequence 3068, App
15	45	75.0	21	4	US-10-293-418-3068 Sequence 3068, App
16	45	75.0	117	6	US-11-009-731-47 Sequence 47, App
17	45	75.0	135	5	US-10-783-311-271 Sequence 271, App
18	45	75.0	256	3	US-09-880-748-1600 Sequence 1600, App
19	45	75.0	256	4	US-10-293-418-1600 Sequence 1600, App
20	44	73.3	16	3	US-09-880-748-2129 Sequence 2129, App
21	44	73.3	16	4	US-10-293-418-2129 Sequence 2129, App
22	44	73.3	17	3	US-09-880-748-2876 Sequence 2876, App
23	44	73.3	17	4	US-10-293-418-2876 Sequence 2876, App
24	44	73.3	18	5	US-10-984-960A-8 Sequence 8, App
25	44	73.3	117	4	US-10-041-860-206 Sequence 206, App
26	44	73.3	123	4	US-10-309-762-18 Sequence 18, App
27	44	73.3	123	4	US-10-309-762-18 Sequence 19, App

28	44	73.3	124	4	US-10-292-088-106 Sequence 106, App
29	44	73.3	127	4	US-10-041-860-31 Sequence 243, App
30	44	73.3	127	4	US-10-041-860-243 Sequence 325, App
31	44	73.3	127	4	US-10-041-860-325 Sequence 42, App
32	44	73.3	127	4	US-10-665-383-42 Sequence 42, App
33	44	73.3	127	4	US-10-466-242-53 Sequence 2, App
34	44	73.3	127	5	US-10-984-960A-2 Sequence 10, App
35	44	73.3	129	4	US-10-292-088-10 Sequence 10, App
36	44	73.3	134	4	US-10-364-743-109 Sequence 109, App
37	44	73.3	134	4	US-10-364-743-110 Sequence 110, App
38	44	73.3	134	5	US-10-452-593-16 Sequence 16, App
39	44	73.3	134	5	US-10-452-593-109 Sequence 109, App
40	44	73.3	134	5	US-10-452-593-110 Sequence 110, App
41	44	73.3	145	5	US-10-644-277-146 Sequence 146, App
42	44	73.3	145	5	US-10-473-287-34 Sequence 34, App
43	44	73.3	157	5	US-10-473-287-63 Sequence 63, App
44	44	73.3	157	5	US-10-473-287-63 Sequence 61, App
45	44	73.3	249	5	US-10-935-290-61 Sequence 61, App

ALIGNMENTS

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RESULT 1
US-10-632-706-126
; Sequence 126, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 126
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-126
Query Match 100.0%; Score 60; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 LATYYFGLDV 11
Db 1 LATYYFGLDV 11
RESULT 2
US-10-632-706-127
; Sequence 127, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 407T-895120US
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806

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;; PRIOR FILING DATE: 1998-08-31
;; NUMBER OF SEQ ID NOS: 278
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 127
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-127

Query Match 100.0%; Score 60; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LATYYFGLDV 11
Db 1 LATYYFGLDV 11

RESULT 3
US-11-031-485-116
;; Sequence 116, Application US/11031485
;; Publication No. US20050232917A1
;; GENERAL INFORMATION:
;; APPLICANT: PULLEN, NICHOLAS
;; APPLICANT: MOLLOY, ELIZABETH
;; APPLICANT: KELLERMAN, SIRID-AIMEE
;; APPLICANT: GREEN, LARRY L.
;; APPLICANT: HAAK-FRENSCH, MARY
;; TITLE OF INVENTION: ANTIBODIES TO MADCAM
;; FILE REFERENCE: ABX-PP6
;; CURRENT APPLICATION NUMBER: US/11/031,485
;; PRIOR FILING DATE: 2005-01-07
;; PRIOR APPLICATION NUMBER: 60/535,490
;; PRIOR FILING DATE: 2004-01-09
;; NUMBER OF SEQ ID NOS: 147
;; SOFTWARE: PatentIn Ver. 3.3
;; SEQ ID NO 116
;; LENGTH: 122
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-031-485-116

Query Match 80.0%; Score 48; DB 6; Length 122;
Best Local Similarity 63.6%; Pred. No. 2.8;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LATYYFGLDV 11
Db 100 VVYYYYGMDV 110

RESULT 4
US-10-364-743-101
;; Sequence 101, Application US/10364743
;; Publication No. US20040009178A1
;; GENERAL INFORMATION:
;; APPLICANT: Bowdish, Katherine S.
;; APPLICANT: Frederickson, Shana
;; APPLICANT: Wild, Martha A.
;; APPLICANT: Maruyama, Toshiaki
;; APPLICANT: No. US20040009178A1an, Mary Jean
;; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
;; FILE REFERENCE: 84 (1087-73)
;; CURRENT APPLICATION NUMBER: US/10/364,743
;; PRIOR FILING DATE: 2003-02-11
;; PRIOR APPLICATION NUMBER: US 60/428,807
;; PRIOR FILING DATE: 2002-11-25
;; NUMBER OF SEQ ID NOS: 118
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 101
;; LENGTH: 129

;; TYPE: PRT
;; ORGANISM: human
US-10-364-743-101

Query Match 78.3%; Score 47; DB 4; Length 129;
Best Local Similarity 77.8%; Pred. No. 4.4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TYYFGLDV 11
Db 105 TYYFGLDV 113

RESULT 5
US-10-452-593-101
;; Sequence 101, Application US/10452593
;; Publication No. US20040258699A1
;; GENERAL INFORMATION:
;; APPLICANT: Bowdish, Katherine S.
;; APPLICANT: Frederickson, Shana
;; APPLICANT: Wild, Martha A.
;; APPLICANT: Maruyama, Toshiaki
;; APPLICANT: Nolan, Mary Jean
;; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
;; FILE REFERENCE: 98 CIP (1087-73 CIP)
;; CURRENT APPLICATION NUMBER: US/10/452,593
;; PRIOR FILING DATE: 2003-06-02
;; PRIOR APPLICATION NUMBER: US 10/364,743
;; PRIOR FILING DATE: 2003-02-11
;; PRIOR APPLICATION NUMBER: US 60/356,086
;; PRIOR FILING DATE: 2002-02-11
;; PRIOR APPLICATION NUMBER: US 60/376,408
;; PRIOR FILING DATE: 2002-04-29
;; PRIOR APPLICATION NUMBER: US 60/428,807
;; PRIOR FILING DATE: 2002-11-25
;; NUMBER OF SEQ ID NOS: 118
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 101
;; LENGTH: 129
;; TYPE: PRT
;; ORGANISM: human
US-10-452-593-101

Query Match 78.3%; Score 47; DB 5; Length 129;
Best Local Similarity 77.8%; Pred. No. 4.4;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TYYFGLDV 11
Db 105 TYYFGLDV 113

RESULT 6
US-10-364-743-15
;; Sequence 15, Application US/10364743
;; Publication No. US20040009178A1
;; GENERAL INFORMATION:
;; APPLICANT: Bowdish, Katherine S.
;; APPLICANT: Frederickson, Shana
;; APPLICANT: Wild, Martha A.
;; APPLICANT: Maruyama, Toshiaki
;; APPLICANT: No. US20040009178A1an, Mary Jean
;; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
;; FILE REFERENCE: 84 (1087-73)
;; CURRENT APPLICATION NUMBER: US/10/364,743
;; PRIOR FILING DATE: 2003-02-11
;; PRIOR APPLICATION NUMBER: US 60/428,807
;; PRIOR FILING DATE: 2002-11-25
;; NUMBER OF SEQ ID NOS: 118
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 15
;; LENGTH: 134
;; TYPE: PRT

ORGANISM: human
US-10-364-743-15

Query Match 78.3%; Score 47; DB 4; Length 134;
Best Local Similarity 77.8%; Pred. No. 4.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYYPGLDV 11
| | | | | | | | | |
Db 110 TTYYYGMDV 118

RESULT 7
US-10-452-593-15

Sequence 15, Application US/10452593
Publication No. US20040258699A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: Frederickson, Shana
APPLICANT: Wild, Martha A.
APPLICANT: Maruyama, Toshiaki
APPLICANT: Nolan, Mary Jean
TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
FILE REFERENCE: 98 CIP (1087-73 CIP)
CURRENT APPLICATION NUMBER: US/10/452,593
CURRENT FILING DATE: 2003-06-02
PRIOR APPLICATION NUMBER: US 10/364,743
PRIOR FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US 60/356,086
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/376,408
PRIOR FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: US 60/428,807
PRIOR FILING DATE: 2002-11-25
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.2
SEQ ID NO 15
LENGTH: 134
TYPE: PRT
ORGANISM: human
US-10-452-593-15

Query Match 78.3%; Score 47; DB 5; Length 134;
Best Local Similarity 77.8%; Pred. No. 4.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYYPGLDV 11
| | | | | | | | | |
Db 110 TTYYYGMDV 118

RESULT 8
US-11-031-485-56

Sequence 56, Application US/11031485
Publication No. US20050232917A1
GENERAL INFORMATION:
APPLICANT: PULLEN, NICHOLAS
APPLICANT: MOLLOY, ELIZABETH
APPLICANT: KELLERMANN, SIRID-AIMEE
APPLICANT: GREEN, LARRY L.
APPLICANT: HAAK-FRENDSCHO, MARY
TITLE OF INVENTION: ANTIBODIES TO MADCAM
FILE REFERENCE: ABX-PF6
CURRENT APPLICATION NUMBER: US/11/031,485
CURRENT FILING DATE: 2005-01-07
PRIOR APPLICATION NUMBER: 60/535,490
PRIOR FILING DATE: 2004-01-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 56
LENGTH: 468
TYPE: PRT
ORGANISM: Homo sapiens

US-11-031-485-56

Query Match 78.3%; Score 47; DB 6; Length 468;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYYPGLDV 11
| | | | | | | | | |
Db 123 TTYYYGMDV 131

RESULT 9
US-11-031-485-18

Sequence 18, Application US/11031485
Publication No. US20050232917A1
GENERAL INFORMATION:
APPLICANT: PULLEN, NICHOLAS
APPLICANT: MOLLOY, ELIZABETH
APPLICANT: KELLERMANN, SIRID-AIMEE
APPLICANT: GREEN, LARRY L.
APPLICANT: HAAK-FRENDSCHO, MARY
TITLE OF INVENTION: ANTIBODIES TO MADCAM
FILE REFERENCE: ABX-PF6
CURRENT APPLICATION NUMBER: US/11/031,485
CURRENT FILING DATE: 2005-01-07
PRIOR APPLICATION NUMBER: 60/535,490
PRIOR FILING DATE: 2004-01-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 18
LENGTH: 469
TYPE: PRT
ORGANISM: Homo sapiens
US-11-031-485-18

Query Match 78.3%; Score 47; DB 6; Length 469;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTYYPGLDV 11
| | | | | | | | | |
Db 123 TTYYYGMDV 131

RESULT 10
US-10-632-706-114

Sequence 114, Application US/10632706
Publication No. US20040175385A1
GENERAL INFORMATION:
APPLICANT: MARKS, JAMES D.
APPLICANT: AMERSDORFER, PETER
TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
FILE REFERENCE: 407T-895120US
CURRENT APPLICATION NUMBER: US/10/632,706
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: US 60/400,721
PRIOR FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 09/144,806
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 114
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: single chain antibody fragment
US-10-632-706-114

Query Match 76.7%; Score 46; DB 4; Length 13;
Best Local Similarity 70.0%; Pred. No. 0.64;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATYYFGLDV 11
| | | | |
Db 4 ANYYYGMDV 13

RESULT 11

US-10-783-311-141
; Sequence 141, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 141
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy Chain amino acid sequence
US-10-783-311-141

Query Match 76.7%; Score 46; DB 5; Length 21;
Best Local Similarity 63.6%; Pred. No. 1;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LATYYFGLDV 11
| | | | |
Db 11 LGNYYYGMDV 21

RESULT 12

US-10-783-311-135
; Sequence 135, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy Chain amino acid sequence
US-10-783-311-135

Query Match 76.7%; Score 46; DB 5; Length 140;
Best Local Similarity 63.6%; Pred. No. 6.9;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LATYYFGLDV 11
| | | | |
Db 109 LGNYYYGMDV 119

RESULT 13

US-10-783-311-277
; Sequence 277, Application US/10783311

; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 277
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heavy Chain amino acid sequence
US-10-783-311-277

Query Match 75.0%; Score 45; DB 5; Length 16;
Best Local Similarity 63.6%; Pred. No. 1.2;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LATYYFGLDV 11
| | | | |
Db 6 VAGYYGMDV 16

RESULT 14

US-09-880-748-3068
; Sequence 3068, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3068
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-3068

Query Match 75.0%; Score 45; DB 3; Length 21;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATYYFGLDV 11
| | | | |
Db 12 APYYGMDV 21

RESULT 15

US-10-293-418-3068
; Sequence 3068, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

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; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3068
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-3068

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Query Match      75.0%; Score 45; DB 4; Length 21;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY      2 ATYYRGLDV 11
        |---|---|
DB      12 APYYYGMDV 21

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 Job time : 80.8333 secs

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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:08:08 ; Search time 3.20833 Seconds
(without alignments)
16.417 Million Cell updates/sec

Title: US-10-632-706-127
Perfect score: 60
Sequence: 1 LATYYFGLDV 11

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Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA New:*
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2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep:*
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7: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pep:*
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*Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	75.0	21	US-11-054-515-3068	Sequence 3068, Ap
2	45	75.0	256	US-11-054-515-1600	Sequence 1600, Ap
3	44	73.3	16	US-11-054-515-2129	Sequence 2129, Ap
4	44	73.3	17	US-11-054-515-2876	Sequence 2876, Ap
5	44	73.3	252	US-11-054-515-1431	Sequence 1431, Ap
6	44	73.3	254	US-11-054-515-3	Sequence 3, Appl
7	44	73.3	254	US-11-054-515-838	Sequence 838, App
8	44	73.3	254	US-11-054-515-870	Sequence 870, App
9	44	73.3	254	US-11-054-515-1287	Sequence 1287, Ap
10	44	73.3	254	US-11-054-515-1288	Sequence 1288, Ap
11	43	71.7	306	US-11-017-550-47	Sequence 47, Appl
12	42	70.0	13	US-11-054-515-3091	Sequence 3091, Ap
13	42	70.0	17	US-11-054-515-2817	Sequence 2817, Ap
14	42	70.0	19	US-11-054-515-2735	Sequence 2735, Ap
15	42	70.0	19	US-11-054-515-2839	Sequence 2839, Ap
16	42	70.0	19	US-11-054-515-2928	Sequence 2928, Ap
17	42	70.0	19	US-11-054-515-2935	Sequence 2935, Ap
18	42	70.0	19	US-11-054-515-3038	Sequence 3038, Ap
19	42	70.0	19	US-11-054-515-3052	Sequence 3052, Ap
20	42	70.0	19	US-11-054-515-3067	Sequence 3067, Ap
21	42	70.0	19	US-11-054-515-3087	Sequence 3087, Ap
22	42	70.0	19	US-11-054-515-3145	Sequence 3145, Ap
23	42	70.0	20	US-11-040-159-4	Sequence 4, Appl
24	42	70.0	20	US-11-054-515-2767	Sequence 2767, Ap
25	42	70.0	20	US-11-054-515-3039	Sequence 3039, Ap

26	42	70.0	24	US-11-054-515-2926	Sequence 2926, Ap
27	42	70.0	124	US-11-144-248-8	Sequence 8, Appl
28	42	70.0	125	US-11-144-248-16	Sequence 16, Appl
29	42	70.0	174	US-11-144-248-4	Sequence 4, Appl
30	42	70.0	248	US-11-054-515-1965	Sequence 1965, Ap
31	42	70.0	248	US-11-054-515-1974	Sequence 1974, Ap
32	42	70.0	251	US-11-054-515-1315	Sequence 1315, Ap
33	42	70.0	251	US-11-054-515-1740	Sequence 1740, Ap
34	42	70.0	251	US-11-054-515-1921	Sequence 1921, Ap
35	42	70.0	252	US-11-054-515-1731	Sequence 1731, Ap
36	42	70.0	253	US-11-054-515-934	Sequence 934, App
37	42	70.0	254	US-11-054-515-1001	Sequence 1001, Ap
38	42	70.0	254	US-11-054-515-1259	Sequence 1259, Ap
39	42	70.0	254	US-11-054-515-1334	Sequence 1334, Ap
40	42	70.0	254	US-11-054-515-1701	Sequence 1701, Ap
41	42	70.0	254	US-11-054-515-1735	Sequence 1735, Ap
42	42	70.0	254	US-11-054-515-1739	Sequence 1739, Ap
43	42	70.0	255	US-11-054-515-1271	Sequence 1271, Ap
44	42	70.0	255	US-11-054-515-1284	Sequence 1284, Ap
45	42	70.0	256	US-11-054-515-1209	Sequence 1209, Ap

ALIGNMENTS

RESULT 1
US-11-054-515-3068
; Sequence 3068, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3068
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3068
Query Match 75.0%; Score 45; DB 7; Length 21;
Best Local Similarity 70.0%; Pred. No. 0.017;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 ATYYFGLDV 11
| | | | |
Db 12 APYYGMDV 21
| | | | |
RESULT 2

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US-11-054-515-1600
; Sequence 1600, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIORITY FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1600
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1600

Query Match          75.0% Score 45; DB 7; Length 256;
Best Local Similarity 70.0%; Pred. No. 0.19;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      2 ATYYFGLDV 11
| | | | |
Db      110 APYYYGMDV 119

RESULT 3
US-11-054-515-2129
; Sequence 2129, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIORITY FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248

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; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2129
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2129

Query Match          73.3% Score 44; DB 7; Length 16;
Best Local Similarity 63.6%; Pred. No. 0.02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 LATYYFGLDV 11
| | | | |
Db      6 LTGYYYGMDV 16

RESULT 4
US-11-054-515-2876
; Sequence 2876, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIORITY FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2876
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2876

Query Match          73.3% Score 44; DB 7; Length 17;
Best Local Similarity 63.6%; Pred. No. 0.02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 LATYYFGLDV 11
| | | | |
Db      7 LTGYYYGMDV 17

RESULT 5
US-11-054-515-1431
; Sequence 1431, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.

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; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1431
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1431

Query Match          73.3%; Score 44; DB 7; Length 252;
Best Local Similarity 63.6%; Pred. No. 0.28;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 LATYYFGADV 11
Db      105 LTGYYYGMDV 115

RESULT 6
US-11-054-515-3
; Sequence 3, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
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; SEQ ID NO 3
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3

Query Match          73.3%; Score 44; DB 7; Length 254;
Best Local Similarity 63.6%; Pred. No. 0.28;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 LATYYFGADV 11
Db      107 LTGYYYGMDV 117

RESULT 7
US-11-054-515-838
; Sequence 838, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 838
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-838

Query Match          73.3%; Score 44; DB 7; Length 254;
Best Local Similarity 63.6%; Pred. No. 0.28;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 LATYYFGADV 11
Db      107 LTGYYYGMDV 117

RESULT 8
US-11-054-515-870
; Sequence 870, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
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PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 870
LENGTH: 254
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Site
LOCATION: (42)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: Site
LOCATION: (45)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: Site
LOCATION: (51)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: Site
LOCATION: (57)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: Site
LOCATION: (67)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: Site
LOCATION: (70)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: Site
LOCATION: (176)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: Site
LOCATION: (192)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: Site
LOCATION: (235)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: Site
LOCATION: (239)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:
NAME/KEY: Site
LOCATION: (240)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-11-054-515-870
Query Match 73.3%; Score 44; DB 7; Length 254;
Best Local Similarity 63.6%; Pred. No. 0.28;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 LATYYRGLDV 11
DB 107 LTGYYYGMDV 117
RESULT 9
US-11-054-515-1287
Sequence 1287, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P3
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1287
LENGTH: 254
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1287
Query Match 73.3%; Score 44; DB 7; Length 254;
Best Local Similarity 63.6%; Pred. No. 0.28;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 LATYYRGLDV 11
DB 107 LTGYYYGMDV 117
RESULT 10
US-11-054-515-1288
Sequence 1288, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P3
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1287
LENGTH: 254
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1287

PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1288
LENGTH: 254
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1288

Query Match 73.3%; Score 44; DB 7; Length 254;
Best Local Similarity 63.6%; Pred. No. 0.28;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTYTFFGLDV 11
Db 107 LTGYTGYGMDV 117

RESULT 11

US-11-017-550-47
Sequence 47, Application US/11017550
Publication No. US20050250183A1
GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
APPLICANT: Schultz, Peter G
APPLICANT: Wang, Lei
APPLICANT: Anderson, John C
APPLICANT: Chin, Jason
APPLICANT: Liu, David R
APPLICANT: Magliery, Thomas
APPLICANT: Meggers, Eric L
APPLICANT: Mehl, Ryan A
APPLICANT: Pasternak, Mirol
APPLICANT: Santoro, Stephen W
APPLICANT: Zhang, Zhiwen
TITLE OF INVENTION: In Vivo Incorporation of Unnatural Amino Acids
FILE REFERENCE: 54-000120US
CURRENT APPLICATION NUMBER: US/11/017,550
CURRENT FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: US/10/126,927
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/285,030
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: US 60/355,514
PRIOR FILING DATE: 2002-02-06
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn version 3.1
SEQ ID NO 47
LENGTH: 306
TYPE: PRT
ORGANISM: Methanococcus jannaschii
US-11-017-550-47

Query Match 71.7%; Score 43; DB 7; Length 306;
Best Local Similarity 77.8%; Pred. No. 0.5;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 TTYTFFGLDV 11
Db 158 TTYTFFGLDV 166

RESULT 12

US-11-054-515-3091
Sequence 3091, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 3091
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-3091

Query Match 70.0%; Score 42; DB 7; Length 13;
Best Local Similarity 75.0%; Pred. No. 0.035;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTYTFFGLDV 11
Db 6 TTYTFFGLDV 13

RESULT 13

US-11-054-515-2817
Sequence 2817, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817

```
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2817
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2817
```

```
Query Match      70.0%; Score 42; DB 7; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.046;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 YYFGGLDV 11
      |||:|:|
Db      10 YYYGMDV 17
```

```
RESULT 14
US-11-054-515-2735
/ Sequence 2735, Application US/11054515
/ Publication No. US20050255532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2735
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2735
```

```
Query Match      70.0%; Score 42; DB 7; Length 19;
Best Local Similarity 75.0%; Pred. No. 0.051;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 YYFGGLDV 11
      |||:|:|
Db      12 YYYGMDV 19
```

```
RESULT 15
US-11-054-515-2899
/ Sequence 2899, Application US/11054515
/ Publication No. US20050255532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2899
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2899
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Query Match      70.0%; Score 42; DB 7; Length 19;
Best Local Similarity 75.0%; Pred. No. 0.051;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY      4 YYFGGLDV 11
      |||:|:|
Db      12 YYYGMDV 19
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Search completed: December 4, 2005, 04:37:48
Job time : 3.20833 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:07:28 ; Search time 78.8333 Seconds
(without alignments)
58.302 Million cell updates/sec

Title: US-10-632-706-128

Perfect score: 66
Sequence: 1 GPMELVGYFDS 11

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*

- 1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/prodata/1/pubppaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/prodata/1/pubppaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	11	US-10-632-706-128	Sequence 128, App
2	45	68.2	230	US-10-156-761-9341	Sequence 9341, App
3	44	66.7	306	US-10-282-122A-73455	Sequence 73455, A
4	44	66.7	367	US-10-282-122A-74966	Sequence 74966, A
5	44	66.7	367	US-10-282-122A-75801	Sequence 75801, A
6	42	63.6	381	US-10-437-963-192224	Sequence 192224, A
7	41	62.1	125	US-10-425-115-253365	Sequence 253365, A
8	41	62.1	171	US-10-424-599-186545	Sequence 186545, A
9	41	62.1	475	US-10-282-122A-48377	Sequence 48377, A
10	41	62.1	475	US-10-437-963-187947	Sequence 187947, A
11	41	62.1	792	US-10-481-032A-252	Sequence 252, App
12	41	62.1	1352	US-11-097-143-29418	Sequence 29418, A
13	40	60.6	50	US-10-424-599-182764	Sequence 182764, A
14	40	60.6	78	US-10-425-115-316649	Sequence 316649, A
15	40	60.6	146	US-10-477-927-21	Sequence 21, App1
16	40	60.6	160	US-10-425-115-333207	Sequence 333207, A
17	40	60.6	477	US-10-425-114-70098	Sequence 70098, A
18	40	60.6	507	US-10-424-599-229226	Sequence 229226, A
19	40	60.6	891	US-10-425-115-229314	Sequence 229314, A
20	40	60.6	931	US-10-732-923-22388	Sequence 22388, A
21	40	60.6	949	US-10-732-923-22387	Sequence 22387, A
22	40	60.6	1355	US-10-437-963-110486	Sequence 110486, A
23	39.5	59.8	511	US-10-425-114-52508	Sequence 52508, A
24	39	59.1	118	US-10-424-599-197468	Sequence 197468, A
25	39	59.1	207	US-10-424-599-163986	Sequence 163986, A
26	39	59.1	235	US-10-732-923-22418	Sequence 22418, A
27	39	59.1	460	US-10-424-599-224678	Sequence 224678, A

ALIGNMENTS

28	39	59.1	522	4	US-10-437-963-194057	Sequence 194057, A
29	39	59.1	537	5	US-10-732-930-10546	Sequence 10546, A
30	39	59.1	658	4	US-10-437-963-121136	Sequence 121136, A
31	39	59.1	670	4	US-10-282-122A-46814	Sequence 46814, A
32	39	59.1	696	5	US-10-450-763-50763	Sequence 50763, A
33	39	59.1	949	5	US-10-732-923-22382	Sequence 22382, A
34	39	59.1	949	5	US-10-732-923-22383	Sequence 22383, A
35	39	59.1	954	4	US-10-437-963-204079	Sequence 204079, A
36	39	59.1	1199	4	US-10-437-963-121132	Sequence 121132, A
37	39	59.1	1441	4	US-10-437-963-111662	Sequence 111662, A
38	38	57.6	48	3	US-09-764-891-3713	Sequence 3713, App
39	38	57.6	71	4	US-10-425-115-277808	Sequence 277808, A
40	38	57.6	84	4	US-10-437-963-150254	Sequence 150254, A
41	38	57.6	96	4	US-10-437-963-141911	Sequence 141911, A
42	38	57.6	135	4	US-10-424-599-205846	Sequence 205846, A
43	38	57.6	167	4	US-10-767-701-60011	Sequence 60011, A
44	38	57.6	185	4	US-10-424-599-230098	Sequence 230098, A
45	38	57.6	207	4	US-10-425-114-53925	Sequence 53925, A

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RESULT 1
US-10-632-706-128
; Sequence 128, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 4077-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; CURRENT FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 128
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-128

Query Match      100.0%; Score 66; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00072;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPMELVGYFDS 11
      |||||
Db      1 GPMELVGYFDS 11

RESULT 2
US-10-156-761-9341
; Sequence 9341, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761

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; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9341
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9341
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Query Match      68.2% Score 45; DB 4; Length 290;
Best Local Similarity 77.8% Pred. No. 38;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```

Qy      3  WELVGYFDS 11
        |||
Db      171 WMLIGYFDS 179
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RESULT 3
US-10-282-122A-73455
; Sequence 73455, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73455
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Salmonella paratyphi A
US-10-282-122A-73455
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Query Match      66.7% Score 44; DB 4; Length 306;
Best Local Similarity 69.2% Pred. No. 58;
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Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
Qy      1  GPWELV----GYF 9
        |||||
Db      66  GPWELVIGPFGYF 78
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RESULT 4
US-10-282-122A-74966
; Sequence 74966, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74966
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Salmonella typhimurium
US-10-282-122A-74966
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Query Match      66.7% Score 44; DB 4; Length 367;
Best Local Similarity 69.2% Pred. No. 69;
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
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Qy      1  GPWELV----GYF 9
        |||||
Db      127 GPWELVIGPFGYF 139
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```

RESULT 5
US-10-282-122A-75801
; Sequence 75801, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
```



```

; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA 034A
; CURRENT FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-23
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-09-06
; PRIOR FILING DATE: 2000-09-06
; PRIOR FILING DATE: 2000-09-09
; PRIOR FILING DATE: 2000-09-09
; PRIOR FILING DATE: 2000-10-23
; PRIOR FILING DATE: 2000-10-23
; PRIOR FILING DATE: 2000-11-27
; PRIOR FILING DATE: 2000-11-27
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2000-12-22
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2001-02-16
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75801
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Salmonella typhi
US-10-282-122A-75801

Query Match          66.7%; Score 44; DB 4; Length 367;
Best Local Similarity 69.2%; Pred. No. 69;
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 GPELVY---GYF 9
DB 127 GPELVYLGPFYF 139

RESULT 6
US-10-437-963-192224
; Sequence 192224, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221) B
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 192224
; LENGTH: 381
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; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_88472C.1.pep
US-10-437-963-192224

Query Match          63.6%; Score 42; DB 4; Length 381;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPELVGY 8
DB 176 GPELVGYF 183

RESULT 7
US-10-425-115-253365
; Sequence 253365, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222) B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 253365
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_16264C.1.pep
US-10-425-115-253365

Query Match          62.1%; Score 41; DB 4; Length 125;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPELVGYF 9
DB 75 GPELVGYF 83

RESULT 8
US-10-424-599-186545
; Sequence 186545, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223) B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 186545
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_139463C.1.pep
US-10-424-599-186545

Query Match          62.1%; Score 41; DB 4; Length 171;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 GPMELVGYFD 10
|||: |||
Db 14 GPMDEMKYFD 23

RESULT 9
US-10-282-122A-48377
; Sequence 48377, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Lianou
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zykend, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48377
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Bacteroides fragilis
; US-10-282-122A-48377

Query Match 62.1%; Score 41; DB 4; Length 475;
Best Local Similarity 54.5%; Pred. No. 2.7e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPMELVGYFD 11
|||: |||
Db 404 GPMKLIYYDS 414

RESULT 10
US-10-437-963-187947
; Sequence 187947, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei
; APPLICANT: Mu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 187947
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(475)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_845C.1.pep
; US-10-437-963-187947

Query Match 62.1%; Score 41; DB 4; Length 475;
Best Local Similarity 70.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPMELVGYFD 10
|||: |||
Db 115 GPMGKGYHD 124

RESULT 11
US-10-481-032A-252
; Sequence 252, Application US/10481032A
; Publication No. US2005017901A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Cheng, Menglong
; APPLICANT: Briggs, Steven
; APPLICANT: Cooper, Bret
; APPLICANT: Goff, Stephen A.
; APPLICANT: Moushaher, Todd
; APPLICANT: Glazebrook, Jane
; APPLICANT: Katagiri, Fumitaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provate, Nicolas
; APPLICANT: Rieke, Darrell
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 60148USPCT
; CURRENT APPLICATION NUMBER: US/10/481,032A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/300,112
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/342,327
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/IB02/02450
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 1201
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 252
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(14)
; OTHER INFORMATION: Xaa = any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)..(16)
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OTHER INFORMATION: Xaa = any naturally occurring amino acid
FEATURE:
NAME/KEY: misc_feature
LOCATION: (399)..(399)
OTHER INFORMATION: Xaa = any naturally occurring amino acid
FEATURE:
NAME/KEY: misc_feature
LOCATION: (493)..(493)
OTHER INFORMATION: Xaa = any naturally occurring amino acid
FEATURE:
NAME/KEY: misc_feature
LOCATION: (669)..(669)
OTHER INFORMATION: Xaa = any naturally occurring amino acid
FEATURE:
NAME/KEY: misc_feature
LOCATION: (671)..(671)
OTHER INFORMATION: Xaa = any naturally occurring amino acid
FEATURE:
NAME/KEY: misc_feature
LOCATION: (673)..(673)
OTHER INFORMATION: Xaa = any naturally occurring amino acid
US-10-481-032A-252

Query Match 62.1%; Score 41; DB 5; Length 792;
Best Local Similarity 66.7%; Pred. No. 4.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 PMELVGYFD 10
||:|:|:|
Db 245 PMQLGYCD 253

RESULT 12
US-11-097-143-29418
; Sequence 29418, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 4308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29418
; LENGTH: 1352
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-29418

Query Match 62.1%; Score 41; DB 6; Length 1352;
Best Local Similarity 77.8%; Pred. No. 7.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 WELVGFPS 11
|:|:|:|:|
Db 161 WRNVGFPS 169

RESULT 13
US-10-424-599-182764
; Sequence 182764, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 182764
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_13604C.1.pep
US-10-424-599-182764

Query Match 60.6%; Score 40; DB 4; Length 50;
Best Local Similarity 66.7%; Pred. No. 48;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 GPMELVGYF 9
|:|:|:|:|
Db 32 GKMKLVGYF 40

RESULT 14
US-10-425-115-319649
; Sequence 319649, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 319649
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_54590C.1.pep
US-10-425-115-319649

Query Match 60.6%; Score 40; DB 4; Length 78;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GPMELVGYF 9
|:|:|:|:|
Db 21 GPMVLAGWF 29

RESULT 15
US-10-477-527-21
; Sequence 21, Application US/10477527
; Publication No. US20040171807A1

```

; GENERAL INFORMATION:
; APPLICANT: The Trustees of the University of Pennsylvania
; APPLICANT: Gao, Guangping
; APPLICANT: Mieson, James M.
; TITLE OF INVENTION: Method for Rapid Screening of Bacterial Transformants and Novel S
; FILE REFERENCE: UPN-N2630PCT
; CURRENT APPLICATION NUMBER: US/10/477,527
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/300,501
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/385,632
; PRIOR FILING DATE: 2002-06-04
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 146
; TYPE: PRT
; ORGANISM: chimpanzee C68 adenovirus protein
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (62) .. (62)
; OTHER INFORMATION: Xaa can be any amino acid
US-10-477-527-21

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Query Match      60.6%; Score 40; DB 4; Length 146;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 GPWELVG 7
        |||:|
Db      101 GPWEYVG 107

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Search completed: December 4, 2005, 04:37:29
 Job time : 79.8333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 03:59:51 ; Search time 23.6042 Seconds
(without alignments)
38.528 Million cell updates/sec

Title: US-10-632-706-128
Perfect score: 66
Sequence: 1 GPMELVGYFDS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	62.1	12	1	US-08-264-093-17
2	41	62.1	121	1	US-08-264-093-3
3	39	59.1	274	2	US-09-502-540-14253
4	38	57.6	332	2	US-09-561-763-5
5	38	57.6	332	2	US-09-431-367B-5
6	38	57.6	493	2	US-09-949-016-10836
7	38	57.6	1207	2	US-09-976-594-4
8	37	56.1	427	2	US-09-902-540-15261
9	37	56.1	464	2	US-09-543-681A-6615
10	36	54.5	132	2	US-09-311-021-162
11	36	54.5	140	2	US-09-698-341-29
12	36	54.5	174	2	US-09-902-540-13916
13	36	54.5	194	1	US-08-260-202A-15
14	36	54.5	194	1	US-08-260-202A-24
15	36	54.5	194	1	US-08-017-114-15
16	36	54.5	194	1	US-08-017-114-15
17	36	54.5	194	1	US-08-505-307-15
18	36	54.5	194	2	US-08-505-307-17
19	36	54.5	194	2	US-09-609-151A-15
20	36	54.5	194	2	US-09-609-151A-17
21	36	54.5	194	4	PCT-US94-02034-15
22	36	54.5	194	4	PCT-US94-02034-17
23	36	54.5	206	2	US-09-902-540-16467
24	36	54.5	235	2	US-09-252-991A-29814
25	36	54.5	266	2	US-09-252-991A-21116
26	36	54.5	321	2	US-09-134-000C-3783
27	36	54.5	500	2	US-09-538-092-831

28	36	54.5	521	2	US-09-221-294-2	Sequence 2, Appl1
29	36	54.5	589	2	US-09-489-039A-8395	Sequence 8395, Ap
30	36	54.5	710	2	US-09-518-550-28	Sequence 28, Appl
31	36	54.5	729	2	US-10-104-047-3450	Sequence 3450, Ap
32	36	54.5	751	2	US-09-252-991A-22770	Sequence 22770, A
33	36	54.5	792	2	US-09-994-192-2	Sequence 4, Appl1
34	36	54.5	797	2	US-09-994-192-4	Sequence 4, Appl1
35	36	54.5	1542	2	US-09-949-016-9215	Sequence 9215, Ap
36	36	54.5	3177	1	US-08-477-451-4	Sequence 4, Appl1
37	36	54.5	5332	2	US-09-914-286-6	Sequence 6, Appl1
38	35	53.0	61	2	US-08-978-741-3	Sequence 3, Appl1
39	35	53.0	61	2	US-09-333-729A-5	Sequence 45, Appl
40	35	53.0	99	2	US-09-390-134B-45	Sequence 13948, A
41	35	53.0	142	2	US-09-902-540-13948	Sequence 7, Appl1
42	35	53.0	160	2	US-09-668-673B-7	Sequence 7, Appl1
43	35	53.0	160	2	US-10-389-532-7	Sequence 7, Appl1
44	35	53.0	166	2	US-09-302-626B-52	Sequence 52, Appl
45	35	53.0	166	2	US-09-303-518D-886	Sequence 886, App

ALIGNMENTS

RESULT 1
US-08-264-093-17
Sequence 17, Application US/08264093
Patent No. 5639863
GENERAL INFORMATION:
APPLICANT: Michael D. Dan
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Ridout & Maybee
STREET: 2300 Richmond-Adelaide Centre
STREET: 101 Richmond Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 2J7
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 6.00
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,093
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA: No. 5639863 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 868-1482
TELEFAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: not applicable
TOPOLOGY: linear
US-08-264-093-17
Query Match
Best Local Similarity 62.1%; Score 41; DB 1; Length 12;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GPMELVGYFDS 10
Db 2 GWMIDLNYFD 11

RESULT 2

US-08-264-093-3
Sequence 3, Application US/08264093
Patent No. 5639863
GENERAL INFORMATION:
APPLICANT: Michael D. Dan
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ridout & Maybee
STREET: 2300 Richmond-Adelaide Centre
STREET: 101 Richmond Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 2J7
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 6.00
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,093
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA: No. 5639863 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081
REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 868-1482
TELEFAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 121 amino acids
TYPE: amino acid
STRANDEDNESS: not applicable
TOPOLOGY: linear
US-08-264-093-3

Query Match

Best Local Similarity 62.1%; Score 41; DB 1; Length 121;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPMELVGYD 10

DB 100 GVMDLNLYFD 109

RESULT 3

US-09-902-540-14253
Sequence 14253, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 14253
LENGTH: 274
TYPE: PRT

ORGANISM: Myxococcus xanthus
US-09-902-540-14253

Query Match

Best Local Similarity 59.1%; Score 39; DB 2; Length 274;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 MELVGYFDS 11

DB 153 WMLKGYFDT 161

RESULT 4

US-09-561-763-5
Sequence 5, Application US/09561763
Patent No. 6664373
GENERAL INFORMATION:
APPLICANT: Curtiss, Rory A.J. et al.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
FILE REFERENCE: NMI-074CP2
CURRENT APPLICATION NUMBER: US/09/561,763
PRIOR FILING DATE: 2000-04-29
PRIOR APPLICATION NUMBER: 09/431,367
PRIOR FILING DATE: 01-11-1999
PRIOR APPLICATION NUMBER: US 09/259,951
PRIOR FILING DATE: 01-03-1999
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 332
TYPE: PRT
ORGANISM: Homo sapiens
US-09-561-763-5

Query Match

Best Local Similarity 57.6%; Score 38; DB 2; Length 332;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPMELVGYF 9

DB 99 GRMELVGSF 107

RESULT 5

US-09-431-367B-5
Sequence 5, Application US/09431367B
Patent No. 6670149
GENERAL INFORMATION:
APPLICANT: Curtiss, Rory A.J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
FILE REFERENCE: NMI-074CP
CURRENT APPLICATION NUMBER: US/09/431,367B
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 09/259,951
PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 332
TYPE: PRT
ORGANISM: Homo sapiens
US-09-431-367B-5

Query Match

Best Local Similarity 57.6%; Score 38; DB 2; Length 332;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPMELVGYF 9

DB 99 GRMELVGSF 107

RESULT 6

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US-09-949-016-10836
; Sequence 10836, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10836
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10836

Query Match      57.6%; Score 38; DB 2; Length 493;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2  PWEVGYFDS 11
Db      69  PWTXYDFDN 78

RESULT 7
US-09-976-594-4
; Sequence 4, Application US/0976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 1207
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: incyte ID No. 6673549 1863336CD1
US-09-976-594-4

Query Match      57.6%; Score 38; DB 2; Length 1207;
Best Local Similarity 77.8%; Pred. No. 3.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GPWEVGYGF 9
Db      389  GPTEAVGYGF 397

RESULT 8
US-09-902-540-15261
; Sequence 15261, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: MYXOCOCCUS XANTHUS Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15261
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-15261

Query Match      56.1%; Score 37; DB 2; Length 427;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1  GPWEVGYGF 9
Db      82  GPFSEVGYGF 90

RESULT 9
US-09-543-681A-6615
; Sequence 6615, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6615
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6615

Query Match      56.1%; Score 37; DB 2; Length 484;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      3  WELVGYFDS 11
Db      155  WALIGYQS 163

RESULT 10
US-09-311-021-162
; Sequence 162, Application US/09311021
; Patent No. 6706869
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Reichel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6300-11A
; CURRENT APPLICATION NUMBER: US/09/311,021
; CURRENT FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 162
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-311-021-162

Query Match 54.5%; Score 36; DB 2; Length 132;
Best Local Similarity 55.6%; Pred. No. 59;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPMELVGYF 9
Db 121 GPMQDLPYF 129

RESULT 11

US-09-698-341-29
; Sequence 29, Application US/09698341
; Patent No. 6946273
; GENERAL INFORMATION:
; APPLICANT: Sorge, Joseph
; APPLICANT: Hubert Hogrefe, Holly
; APPLICANT: Conlie, Hansen
; TITLE OF INVENTION: Compositions and Methods Utilizing DNA Polymerases
; FILE REFERENCE: 25436/1560
; CURRENT APPLICATION NUMBER: US/09/698,341
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: 60/162,600
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Thermococcus sp. JDF-3
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (92) ..(92)
; OTHER INFORMATION: X = Unknown
US-09-698-341-29

Query Match 54.5%; Score 36; DB 2; Length 140;
Best Local Similarity 50.0%; Pred. No. 63;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPMELVGYF 10
Db 55 GPMQDLPYF 64

RESULT 12

US-09-902-540-13916
; Sequence 13916, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13916
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13916

Query Match 54.5%; Score 36; DB 2; Length 174;
Best Local Similarity 85.7%; Pred. No. 81;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LVGYFDS 11

Db 6 LVGYFDS 12

RESULT 13

US-08-260-202A-15
; Sequence 15, Application US/08260202A
; Patent No. 5573910
; GENERAL INFORMATION:
; APPLICANT: Derecic, Vojo
; APPLICANT: Martin, Daniel W.
; TITLE OF INVENTION: DETECTION OF CONVERSION TO MUCOIDY IN
; TITLE OF INVENTION: PSEUDOMONAS AERUGINOSA INFECTING CYSTIC FIBROSIS PATIENTS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/260,202A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,202
; FILING DATE: 15-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/017,114
; FILING DATE: 12-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hodgins, Daniel S.
; REGISTRATION NUMBER: 31,026
; REFERENCE/DOCKET NUMBER: UTSK:221\HOD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-260-202A-15

Query Match 54.5%; Score 36; DB 1; Length 194;
Best Local Similarity 71.4%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPMELVGY 7
Db 81 GPMRWVG 87

RESULT 14

US-08-260-202A-24
; Sequence 24, Application US/08260202A
; Patent No. 5573910
; GENERAL INFORMATION:
; APPLICANT: Derecic, Vojo
; APPLICANT: Martin, Daniel W.
; TITLE OF INVENTION: DETECTION OF CONVERSION TO MUCOIDY IN
; TITLE OF INVENTION: PSEUDOMONAS AERUGINOSA INFECTING CYSTIC FIBROSIS PATIENTS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433

CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/260,202A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,202
FILING DATE: 15-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/017,114
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hodgins, Daniel S.
REGISTRATION NUMBER: 31,026
REFERENCE/DOCKET NUMBER: UTSK:221\HOD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-260-202A-24

Query Match 54.5% Score 36; DB 1; Length 194;
Best Local Similarity 71.4%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVG 7
|||:|
DB 81 GPMRWVG 87

RESULT 15
US-08-017-114-15
Sequence 15, Application US/08017114
Patent No. 5591838
GENERAL INFORMATION:
APPLICANT: Detetic, Vojo
APPLICANT: Martin, Daniel W.
TITLE OF INVENTION: DETECTION OF CONVERSION TO MUCOIDY IN
TITLE OF INVENTION: PSEUDOMONAS AERUGINOSA INFECTING CYSTIC FIBROSIS PATIENTS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/017,114
FILING DATE: 19930212
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hodgins, Daniel S.
REGISTRATION NUMBER: 31,026
REFERENCE/DOCKET NUMBER: UTSK:205/HOD

TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/320-7200
TELEFAX: 512/474-7577
TELEX: N/A
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-017-114-15

Query Match 54.5% Score 36; DB 1; Length 194;
Best Local Similarity 71.4%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVG 7
|||:|
DB 81 GPMRWVG 87

Search completed: December 4, 2005, 04:09:43
Job time : 23.6042 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 4, 2005, 04:31:36 ; Search time 100.375 Seconds
(without alignments)
77.318 Million cell updates/sec

Title: US-10-632-706-128
Perfect score: 66
Sequence: 1 GPMELVGYFDS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	68.2	279	2	087858_STRCO
2	45	68.2	290	2	082M58_STRAM
3	45	68.2	748	2	05NQ32_ZYMMO
4	44	66.7	367	1	MECA_SALTY
5	44	66.7	367	1	MECA_SALTY
6	44	66.7	367	2	05PKK1_SALPA
7	44	66.7	449	2	063M53_BURPS
8	43	65.2	231	2	04K719_PSEFS
9	43	65.2	1201	2	07UYR6_RHOBA
10	43	65.2	1633	1	YPT4_CABL
11	43	65.2	7548	2	05WRU1_CABL
12	42	63.6	272	2	0748S8_GBSOL
13	42	63.6	381	2	06K1T5_ORYSA
14	42	63.6	454	2	08TUV9_METAC
15	42	63.6	578	2	08D959_VIBVU
16	42	63.6	578	2	07MLB3_VIBVU
17	42	63.6	1275	2	080061_METMA
18	41	62.1	211	2	08KAK7_PSEAE
19	41	62.1	241	2	082347_ARATH
20	41	62.1	273	2	07UND8_RHOBA
21	41	62.1	318	2	04KEFO_PSEFS
22	41	62.1	491	1	GLNA_ARCFU
23	41	62.1	518	2	05LH40_BACRN
24	41	62.1	518	2	064XZ7_BACRN
25	41	62.1	613	2	06BTL3_DBBHA
26	41	62.1	619	1	GCRR_XENLA
27	41	62.1	619	2	05SKAS_THERR
28	41	62.1	619	2	06PAK3_XENLA
29	41	62.1	697	1	Y2336_MYCTU
30	41	62.1	697	1	Y2353_MYCBO
31	41	62.1	1350	2	09V5J7_DROME

32	41	62.1	1370	2	07K0X6_DROME
33	41	62.1	2581	2	07T7T5_YVIRU
34	40	60.6	122	2	08B357_SHEON
35	40	60.6	146	2	08UY74_SHEON
36	40	60.6	206	2	06CP97_9ADEN
37	40	60.6	207	2	06CPD3_9ADEN
38	40	60.6	208	2	06CPG9_9ADEN
39	40	60.6	210	2	06H1B6_9ADEN
40	40	60.6	210	2	08BEL6_ADE04
41	40	60.6	382	2	07N9W4_PROL
42	40	60.6	304	2	087XQ4_PSESM
43	40	60.6	319	2	04ZPN4_PSESY
44	40	60.6	323	2	04INB2_GIBZE
45	40	60.6	392	2	08LR17_PETHY
					07KQX6_drosophila
					07T7T5_heterosigma
					08B357_sheanella
					08UY74_simian aden
					06CP97_simian aden
					06CPD3_simian aden
					06CPG9_simian aden
					06H1B6_human aden
					08BEL6_human aden
					07N9W4_photobacter
					087XQ4_pseudomonas
					04ZPN4_pseudomonas
					04INB2_gibberella
					08LR17_pecunia hyb

ALIGNMENTS

```

RESULT 1
087858_STRCO      PRT; 279 AA.
AC 087858;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE Putative transmembrane sugar transport protein.
GN OrderedLocustNames=SC06603; ORFNames=SC8A6.24;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OK NCBI_TaxId=1902;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A3(2) / M145;
RX MEDLINE=2196410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleiser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleiser T., Larke L., Murphree K., O'Neill S.,
RA Rabbinowitch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RL coelicolor A3(2).";
CC Nature 417:141-147(2002).
CC -I- FUNCTION: Part of a binding-protein-dependent transport system.
CC -I- Probably responsible for the translocation of the substrate across
CC -I- the membrane (By similarity).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -I- SIMILARITY: Belongs to the binding-protein-dependent transport
CC -I- system permease family.
CC EMBL AL939128; CA19796.1; -; Genomic_DNA.
DR PIR: T35791; T35791.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0016020; C: membrane; IEA.
DR GO: GO:0005351; F: sugar porter activity; IEA.
DR GO: GO:0005215; F: transporter activity; IEA.
DR GO: GO:0006810; P: transport; IEA.
DR InterPro: IPR000515; BPD_transp.
DR Pfam: PF00528; BPD_transp_1; 1.
DR PROSITE: PS50928; ABC_TM1; 1.
KW Complete proteome; Sugar transport; Transmembrane; Transport.
SQ
SEQUENCE 279 AA; 30335 MW; 88606338588F8BFA CRC64;
Query Match 68.2%; Score 45; DB 2; Length 279;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 MELVGYFDS 11
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Db          160 WMLIGYFDS 168

RESULT 2
ID Q82M58_STRAM PRELIMINARY; PRT; 290 AA.
AC Q82M58;
DT 01-JUN-2003 (TREMblrel. 24, Created)
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
DE 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Putative sugar ABC transporter permease protein.
GN OrderedLocuNames=SAV1802;
OS Streptomyces avermectilis.
OC Streptomyces; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomyces; Streptomyces; Streptomyces.
OX NCBI_TaxID=33903;

RM NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.21143198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shirose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermectilis: deducing the ability of producing secondary
RT metabolites."
RT Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562; DOI=10.1038/nbt820;
RA Ikeda H., Ishikawa J., Hanamoto A., Shirose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermectilis."
RT Nat. Biotechnol. 21:526-531(2003).
CC -1- FUNCTION: Part of a binding-protein-dependent transport system.
CC Probably responsible for the translocation of the substrate across
CC the membrane (by similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
CC -1- SIMILARITY: Belongs to the binding-protein-dependent transport
CC system permease family.
DR EMBL; BA000030; BAC69513.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005351; F:sugar porter activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR InterPro; IPR00515; BPD transp.
DR Pfam; PF00528; BPD transp. 1.
DR PROSITE; PS50928; ABC TM1. 1.
DR Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 290 AA; 31323 MW; 92650429419A5B9 CRC64;

Query Match 68.2%; Score 45; DB 2; Length 290;
Best Local Similarity 77.8%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy          3 WELVGYFDS 11
Db          171 WMLIGYFDS 179

RESULT 3
ID Q5NQ32_ZYMO PRELIMINARY; PRT; 748 AA.
AC Q5NQ32;
DT 01-FEB-2005 (TREMblrel. 29, Created)
DT 01-FEB-2005 (TREMblrel. 29, Last sequence update)
DE 01-FEB-2005 (TREMblrel. 29, Last annotation update)
DE Polyribonucleotide nucleosidyltransferase (EC 2.7.7.8).
GN Name=pnp; OrderedLocuNames=ZMO0549;
OS Zymomonas mobilis.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Zymomonas.
OX NCBI_TaxID=542;

RM NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 31821 / ZM4 / CP4;
RX PubMed=15592456; DOI=10.1038/nbt1045;
RA Seo J.-S., Chong H., Park H.S., Yoon K.-O., Jung C., Kim J.J.,
RA Hong J.H., Kim H., Kim J.-H., Kil J.-I., Park C.J., Oh H.-M.,
RA Lee J.-S., Jin S.-U., Um H.-W., Lee H.-O., Oh S.-O., Kim J.Y.,
RA Kang H.L., Lee S.Y., Lee K.J., Kang H.S.;
RT "The genome sequence of the ethanologenic bacterium Zymomonas mobilis
RT ZM4."
RT Nat. Biotechnol. 23:63-68(2005).
RN [1]

RP EMBL; AB008692; AY69173.1; -; Genomic DNA.
RC GO; GO:0000175; F:3'-5'-exoribonuclease activity; IEA.
DR GO; GO:0004654; F:polyribonucleotide nucleosidyltransferase a. .; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006396; P:RNA processing; IEA.
DR InterPro; IPR001247; 3-Exonase.
DR InterPro; IPR004087; KH.
DR InterPro; IPR004088; KH type_1.
DR InterPro; IPR012162; PNPase.
DR InterPro; IPR003029; S1.
DR Pfam; PF00013; KH 1; 1.
DR Pfam; PF03726; PNPase; 1.
DR Pfam; PF01138; RNase PH; 2.
DR Pfam; PF03725; RNase PH_C; 2.
DR Pfam; PF00575; S1; 1.
DR PIRSF; PIRSF005499; PNPase; 1.
DR SMART; SM00322; KH; 1.
DR SMART; SM00316; S1; 1.
DR PROSITE; PS50084; KH type_1; 1.
DR PROSITE; PS50126; S1; 1.
DR Complete proteome; Nucleosidyltransferase; Transferase.
SQ SEQUENCE 748 AA; 81949 MW; EB8C43821F85F6DB CRC64;

Query Match 68.2%; Score 45; DB 2; Length 748;
Best Local Similarity 80.0%; Pred. No. 67;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy          2 PWEIVGYFDS 11
Db          230 PWEIVGYFDS 239

RESULT 4
ID WECA_SALTI STANDARD; PRT; 367 AA.
AC WECA_SALTI
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-MAY-2005 (Rel. 47, Last annotation update)
DE Undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate
DE transferase (EC 2.7.8.-) (UDP-GlcNAc:undecaprenyl-phosphate GlcNAc-1-
DE phosphate transferase).
GN Name=weca; Synonyms=rtf; OrderedLocuNames=STY3637, t3379;
OS Salmomella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmomella.
OX NCBI_TaxID=601;
RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parthali J., Dougan G., James K.D., Thomson N.R., Pickard D., Wein J.,
RA Churcher C.M., Mungall K.V., Bentley S.D., Holden M.T.G., Sebatista M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd U., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jørgen K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,

```

RA	Whitehead S., Barrrell B.G.:	"Complete genome sequence of a multiple drug resistant <i>Salmonella</i>
RT	enterica serovar Typhi CT18."	
RL	Nature 413:848-852(2001).	
RN	(2)	
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	
RC	STRAIN=Ty2 / ATCC 700931;	
RX	MEDLINE=22531367; PubMed=12644504;	
DOI=10.1128/JB.185.7.2330-2337.2003;		
RX	Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,	
RA	Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;	
RT	"Comparative genomics of <i>Salmonella enterica</i> serovar Typhi strains Ty2	
and Ct18".		
RL	J. Bacteriol. 185:2330-2337 (2003).	
CC	-1- FUNCTION: Catalyzes the synthesis of Und-PP-glucNAc (lipid I), the	
CC	first lipid-linked intermediate involved in ECA synthesis. This	
CC	lipid is also an acceptor for the addition of subsequent sugars to	
CC	complete the biosynthesis of O-antigen (By similarity).	
CC	-1- CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + undecaprenyl	
CC	phosphate = UMP + N-acetyl-alpha-D-glucosaminylidiphospho-	
CC	undecaprenol.	
CC	-1- COFACTOR: Magnesium and manganese (By similarity).	
CC	-1- PATHWAY: Synthesis of enterobacterial common antigen (ECA).	
CC	Synthesis of lipopolysaccharide O-antigen.	
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane	
CC	(By similarity).	
CC	-1- SIMILARITY: Belongs to the glycosyltransferase 4 family. Weca	
CC	subfamily.	
CC	-----	
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation --	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use as long as its content is in no way modified and this statement is not	
CC	removed.	
CC	-----	
DR	EMBL, AL637279; CAD09398.1; -; Genomic DNA.	
DR	EMBL, AE016845; AA070903.1; -; Genomic DNA.	
DR	InterPro: IPR001750; ECA_Weca_rel.	
DR	InterPro: IPR001715; Glyco_transf_4.	
DR	Pfam: PF00953; Glycos_transf_4; 1.	
DR	TIGRFAMs: TIGR02380; ECA_weca; 1.	
KM	Complete proteome; Glycosyltransferase; Inner membrane;	
KM	Lipopolysaccharide biosynthesis; Magnesium; Manganese; Membrane;	
KM	Transferase; Transmembrane.	
FT	TRANSMEM 3 23 Potential.	
FT	TRANSMEM 45 65 Potential.	
FT	TRANSMEM 69 89 Potential.	
FT	TRANSMEM 106 126 Potential.	
FT	TRANSMEM 129 149 Potential.	
FT	TRANSMEM 158 178 Potential.	
FT	TRANSMEM 187 207 Potential.	
FT	TRANSMEM 213 233 Potential.	
FT	TRANSMEM 242 262 Potential.	
FT	TRANSMEM 294 314 Potential.	
FT	TRANSMEM 318 338 Potential.	
SEQ	SEQUENCE 367 AA; 41086 MW; 28DA33CBA1E2D930 CRC64;	
QY	Query Match 66.7%; Score 44; DB 1; Length 367;	
Db	Beef Local Similarity 69.2%; Pred. No. 49;	
Matches	9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;	
QY	1 GPMELV---GYF 9	
Db	127 GPMELVLGPGGYF 139	
RESULT 5		
WECA_SALTY		
ID	WECA_SALTY STANDARD; PRT; 367 AA.	
AC	Q9L6R7; O33788;	
DT	28-FEB-2003 (Rel. 41, Created)	
DT	28-FEB-2003 (Rel. 41, Last sequence update)	
DT	10-MAY-2005 (Rel. 47, Last annotation update)	

DE	undecaprenyl-phosphate alpha-N-acetylglucosaminyl 1-phosphate
DE	transferase (EC 2.7.8.-) (UDP-GlcNAc:undecaprenyl-phosphate
DE	phosphate transferase).
GN	Name=wecc; Synonym=rtte; OrderedLocustName=STM3918; ORFName=STM01_72;
OS	Salmonella typhimurium.
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC	Enterobacteriaceae; Salmonella.
OX	NCBI_TaxID=602;
RN	[1]
RP	NCBIENTRY SEQUENCE [LARGE SCALE GENOMIC DNA].
RC	STRAIN=Lt7 / SGSC1412 / ATCC 700720.
RC	MEBLINE=914949259; PubMed=9738879; DOI=10.1007/s004380050787;
RX	MEBLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA	McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA	Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,
RA	Lehman S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA	Ryan B., Sun H., Flores R., Miller W., Stoneking T., Nhan M.,
RA	Waterston R., Wilson R.K.;
RT	"Complete genome sequence of <i>Salmonella enterica</i> serovar Typhimurium
RT	Lt7.";
RL	Nature 413:852-856(2001).
RN	[2]
RP	NCBIENTRY SEQUENCE OF 111-367.
RC	STRAIN=Lt7;
RC	MEBLINE=964092259; PubMed=9738879; DOI=10.1007/s004380050787;
RX	Moussif C., Cano D.A., Casadesu J.;
RA	"The sfxX, rte and metN genes of <i>Salmonella typhimurium</i> and their
RT	involvement in the His(c) pleiotropic response.";
RL	Mol. Genet. 259:46-53(1998).
CC	-1- FUNCTION: Catalyzes the synthesis of Und-pp-GlcNAc (Lipid I), the
CC	first lipid-linked intermediate involved in ECA synthesis. This
CC	lipid is also an acceptor for the addition of subsequent sugars to
CC	complete the biosynthesis of O-antigen (By similarity).
CC	-1- CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + undecaprenyl
CC	phosphate = UMP + N-acetyl-alpha-D-glucosaminylidiphospho-
CC	undecaprenol.
CC	-1- COFACTOR: Magnesium and manganese (By similarity).
CC	-1- ENZYME REGULATION: Inhibited by tunicamycin.
CC	-1- PATHWAY: Synthesis of enterobacterial common antigen (ECA).
CC	Synthesis of lipopolysaccharide O-antigen.
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC	(By similarity).
CC	-1- SIMILARITY: Belongs to the glycosyltransferase 4 family. Wecc
CC	subfamily.
CC	-----
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use as long as its content is in no way modified and this statement is not
CC	removed.
CC	-----
DR	EMBL; AF233324; AAF33469.1; -; Genomic DNA.
DR	EMBL; AE008883; ALA22767.1; -; Genomic DNA.
DR	EMBL; AJ002275; CAA05287.1; -; Genomic DNA.
DR	StyGene; SGT7777; rfe.
DR	InterPro; IPR012750; ECA_wecc_rel.
DR	InterPro; IPR000715; Glyco_transf_4.
DR	Pfam; PF00953; Glycos_transf_4; 1.
DR	TIGRFAMs; TIGR02380; ECA_wecc_4; 1.
KM	Complete proteome; Glycosyltransferase; Inner membrane;
KM	Lipopolysaccharide biosynthesis; Magnesium; Manganese; Membrane;
KM	Transferase; Transmembrane.
FT	TRANSMEM 3 23
FT	TRANSMEM 45 65
FT	TRANSMEM 69 89
FT	TRANSMEM 106 126
FT	TRANSMEM 129 149
FT	TRANSMEM 158 178
FT	TRANSMEM 187 207
FT	TRANSMEM 213 233
FT	TRANSMEM 242 262
FT	TRANSMEM 294 314
FT	TRANSMEM 318 338
FT	CONFLICT 118 120
FT	HMG -> ALS (in Ref. 2).

FT CONFLICT 128 138 PWEVLVGPFGY -> ALGVSNAPLMW (1n Ref. 2).
 FT CONFLICT 146 148 MAA -> LNG (1n Ref. 2).
 FT CONFLICT 220 220 S -> C (1n Ref. 2).
 SQ SEQUENCE 367 AA; 41087 MW; 1EDJ31CB1AE2D938 CRC64;

Query Match 66.7%; Score 44; DB 1; Length 367;
 Best Local Similarity 69.2%; Pred. No. 49;
 Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 GPEWLV----GYF 9
 |||||
 Db 127 GPEWLVGPFGY 139

RESULT 6

OSPK1_SALPA PRELIMINARY; PRT; 367 AA.

AC OSPK1; 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Putative undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase.
 GN Name: rfe; OrderedLocustNames=SPJ3756;
 OS Salmonella paratyphi-a.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=54388;
 RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ATCC 9150;
 RC PubMed=15531882; DOI=10.1038/ng1470;
 RA McClelland M., Sanderson K.R., Clifton S.W., Latreille P., Porwollik S., Sabo A., Meyer R., Bieri T., Oseriky P., McCellan M., Hartins C.R., Wang C., Nguyen C., Berghoff A., Elliott G., Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D., Leonard S., Sun H., Fulton L., Nash W., Miner T., Mink P., Delehaunty K., Fronick C., Magrini V., Nhan M., Warren W., Flores L., Speleth J., Wilson R.K.;
 RT "Comparison of genome degradation in Paratyphi A and Typhi, human-restricted serovars of Salmonella enterica that cause typhoid";
 RL Nat. Genet. 36:1268-1274(2004).
 DR EMBL; CP000026; AAV79540.1; -; Genomic DNA.
 DR GO; GO:0018666; C:inner membrane; IEA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016757; F:transferase activity, transferring glycosyl. . .; IEA.
 DR GO; GO:0006629; P:lipid metabolism; IEA.
 DR GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
 DR InterPro; IPR00715; Glyco_trans_4.
 DR InterPro; IPR001865; Ribosomal_S2.
 DR Pfam; PF00953; Glycos_transf_4; 1.
 DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN 1.
 KM Complete proteome; Glycosyltransferase; Transferase.
 SQ SEQUENCE 367 AA; 41086 MW; 1EDJ31CB1AE2D938 CRC64;

Query Match 66.7%; Score 44; DB 2; Length 367;
 Best Local Similarity 69.2%; Pred. No. 49;

Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 GPEWLV----GYF 9
 |||||
 Db 127 GPEWLVGPFGY 139

RESULT 7
 OS3N53_BURPS PRELIMINARY; PRT; 449 AA.

AC OS3N53; 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=BPS0443;

OS Burkholderia pseudomallei (Pseudomonas pseudomallei).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia; pseudomallei group.
 OX NCBI_TaxID=28450;

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=K96243;
 RC PubMed=15377794; DOI=10.1073/pnas.040302101;
 RA Holden M.T.G., Titchall R.W., Peacock S.D., Cerdano-Tarraga A.-M., Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L., Bentley S.D., Seabright M., Thomson N.R., Bacon N., Beacham I.R., Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I., Chillingworth T., Cronin A., Crosslet B., Davis P., Deshaizer D., RA Felwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagsals K., Kelch K.B., Maddison M., Moule S., Price C., Quail M.A., Rabinowitch E., Rutherford K., Sanders M., Simmonds M., Songvilat S., Stevens K., Tamara S., Vesaratchaveest M., Whitehead S., Yeats C., Barrett B.G., Oyston P.C.F., Parkhill J.;
 RT "Genomic plasticity of the causative agent of melioidosis".
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
 DR EMBL; BX571966; CAH37899.1; -; Genomic DNA.
 KM Complete proteome; Hypothetical protein.
 SQ SEQUENCE 449 AA; 49531 MW; F1618B7466D15240 CRC64;

Query Match 66.7%; Score 44; DB 2; Length 449;
 Best Local Similarity 75.0%; Pred. No. 60;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPEWLVGY 8
 |||||
 Db 183 GPEWLVGY 190

RESULT 8
 Q4K719_PSEFS PRELIMINARY; PRT; 231 AA.

AC Q4K719; 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Phosphoserine phosphatase, putative.
 GN ORFNames=PFL_4883;
 OS Pseudomonas fluorescens (strain Pf-5).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=220664;
 RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=PF-5;
 RC PubMed=15980861; DOI=10.1038/nbt1110;
 RA Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S., Mavrodin D., DeBoy R.T., Sehnadri R., Ren Q., Madupu R., Dodson R.J., Durbin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M., RA Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K., RA Khouri H.M., Pierson B., Pierson L., III, Thomasow L., Loper J.;
 RT "Complete genome sequence of the plant commensal Pseudomonas fluorescens Pf-5";
 RL Nat. Biotechnol. 23:873-878(2005).
 DR EMBL; CP000076; AAY94113.1; -; Genomic DNA.
 SQ SEQUENCE 231 AA; 25717 MW; A4DEA84C59107CF2 CRC64;

Query Match 65.2%; Score 43; DB 2; Length 231;
 Best Local Similarity 80.0%; Pred. No. 46;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PWEVLGYFDS 11
 |||||
 Db 61 PWEVLGYFDS 70

RESULT 9
 Q7UYR6_RHOBA

```

ID 07YUR6_RHOBA PRELIMINARY; PRT; 1201 AA.
AC 07YUR6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocuNames=RB426;
OS Rhodospirillum rubrum.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxId=117;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1;
RA Gloeckner F.O., Kobe M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heilmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1."
RT Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294133; CAD71575.1; -; Genomic_DNA.
DR GO; GO:0020037; F.heme binding; IEA.
DR GO; GO:0006118; P.electron transport; IEA.
DR InterPro; IPR012282; Cytochrome_c_R.
DR InterPro; IPR011444; DUF1549.
DR Pfam; PF07635; PSCytl; 1.
DR Pfam; PF07583; PSCytl2; 1.
DR Pfam; PF07587; PSD1; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1201 AA; 134482 MW; 728682735130D01 CRC64;

Query Match 65.2%; Score 43; DB 2; Length 1201;
Best Local Similarity 72.7%; Pred. No. 2.4e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GPMELVGYFDS 11
DB 1029 GLWEAVGYTDS 1039

RESULT 10
ID YP74_CAEEL STANDARD; PRT; 1633 AA.
AC 009231; Q10908;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Hypothetical protein B0228.4 in chromosome II.
GN ORFNames=B0228.4/B0228.2;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Br1scf1 N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE REVISION.
RG Wormbase consortium;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -----
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CC removed.

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CC EMBL; U23168; AAC38806.2; -; Genomic_DNA.
DR Ensembl; B0228.4; Caenorhabditis elegans.
DR Wormbase; WBGene00015061; B0228.4.
DR WormPep; B0228.4; CB31282.
DR InterPro; IPR010734; Copine.
DR Pfam; PF07002; Copine; 1.
DR PRINTS; PR00453; VWRPDOMAIN.
KW Complete proteome; Hypothetical protein.
FT COMBIAS 155 165
FT COMBIAS 316 338
FT COMBIAS 892 1019
FT COMBIAS 1633 AA; 183328 MW; 3B4EB46800B7A44D CRC64;
SQ SEQUENCE 1633 AA; 183328 MW; 3B4EB46800B7A44D CRC64;

Query Match 65.2%; Score 43; DB 1; Length 1633;
Best Local Similarity 60.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPMELVGYFDS 10
DB 1567 GPMNMGRPD 1576

RESULT 11
ID Q5WRU1_CAEEL PRELIMINARY; PRT; 7548 AA.
AC Q5WRU1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein B0228.4.
GN ORFNames=B0228.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Br1scf1 N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; U23168; AAU87832.1; -; Genomic_DNA.
DR Ensembl; B0228.4; Caenorhabditis elegans.
DR Wormbase; WBGene00015061; B0228.4.
DR WormPep; B0228.4; CB37470.
DR InterPro; IPR010734; Copine.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF07002; Copine; 1.
DR SMART; SM00327; VWA; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 7548 AA; 840584 MW; 8BEC3CC03D12C1C8 CRC64;

Query Match 65.2%; Score 43; DB 2; Length 7548;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPMELVGYFDS 10
DB 7482 GPMNMGRPD 7491

RESULT 12
ID Q748S8_GROSL PRELIMINARY; PRT; 272 AA.
AC Q748S8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Glutamate racemase (EC 5.1.1.3).
GN Name=mult; OrderedLocuNames=GSU2923;

```

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OS Geobacter sulfurreducens.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Geobacteraceae; Geobacter.
OX NCBI_TaxId=35554;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PCA / ATCC 51573;
RX PubMed=14671304; DOI=10.1126/science.1088727;
RA Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
RA Heidelberg J.F., Wu M., Ward N.L., Beaman M.J., Dodson R.J.,
RA Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,
RA Wain M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
RA Davidson T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
RA Velkan A.J.F., Khouri H.M., Feldblyum T.V., Uterback T.R.,
RA Van Aken S.E., Loyley D.R., Fraser C.M.;
RT "Genome of Geobacter sulfurreducens: metal reduction in subsurface
RT environments."
RL Science 302:1967-1969(2003).
DR EMBL, AE017180; AAR36315.1; -; Genomic_DNA.
DR HSSP, P56868; 1B74.
DR TIGR, GSU2923; -.
DR GO; GO:0008881; F:glutamate racemase activity; IEA.
DR GO; GO:0016853; F:isomerase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0009252; P:peptidoglycan biosynthesis; IEA.
DR InterPro; IPR001920; Asp/Glu race.
DR InterPro; IPR004391; Asp/Glu race.
DR Pfam; PF01177; Asp_Glu_race; 1.
DR TIGRfam; TIGR00067; gltC_race; 1.
DR PROSITE; PS00923; ASP_GLU_RACEMASE_1; 1.
DR PROSITE; PS00924; ASP_GLU_RACEMASE_2; 1.
DR Complete proteome; Isomerase.
SQ SEQUENCE 272 AA; 29521 MW; 674BA01437EC4163 CRC64;

Query Match 63.6%; Score 42; DB 2; Length 272;
Best Local Similarity 60.0%; Pred. No. 80;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PWEVLGYFDS 11
DB 2 PMAKIGIFDS 11

RESULT 13
O6K1T5 ORYSA PRELIMINARY; PRT; 381 AA.
AC O6K1T5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein OSUJBA0038P01.38.
GN Name=OSJBA0038P01.38;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhacoidae; Oryzaceae; Oryza.
OX NCBI_TaxId=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GAS) genomic DNA, chromosome 2, BAC
RT clone:OSJBA0038P01.1."
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP006457; BAD22515.1; -; Genomic_DNA.
DR Oryza sativa; O6K1T5; -.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR Hypothetical protein.
SQ SEQUENCE 381 AA; 42714 MW; A50564C2F7224FC4 CRC64;

Query Match 63.6%; Score 42; DB 2; Length 381;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;

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Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVGY 8
DB 176 GPMELTGF 183

RESULT 14
O8TV9 METAC PRELIMINARY; PRT; 454 AA.
AC O8TV9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein MA3668.
GN Ordered locus names=MA3668;
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanocicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxId=2214;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238; DOI=10.1101/gr.223902;
RA Galagan J.E., Nuebaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Altsch D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., Deatellano K., Johnson R.,
RA Linton L., McMan P., McKernan K., Talmas J., Tittel A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Gramme D.A., Guse A.M.,
RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Unayam L.A., White O., White R.H., de Macario E.C.,
RA Perry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,
RA Pritchett M., Sowers K.R., Stanon R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Biren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity."
RL Genome Res. 12:532-542(2002).
DR EMBL, AE011076; AA07023.1; -; Genomic_DNA.
DR InterPro; IPR010180; Cae_CXXC_CXXC.
DR TIGRfam; TIGR01908; cae_CXXC_CXXC; 1.
DR Complete proteome.
SQ SEQUENCE 454 AA; 52893 MW; 28BD6A65629B0A0 CRC64;

Query Match 63.6%; Score 42; DB 2; Length 454;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVGY 9
DB 319 GPMELVGY 327

RESULT 15
O8D959 VIBVU PRELIMINARY; PRT; 578 AA.
AC O8D959;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Methyl-accepting chemotaxis protein.
GN Ordered locus names=VV12747;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxId=672;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6."
RT Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AB016806; AA011091.1; -; Genomic_DNA.
DR HSSP; P02942; 1QU7.
DR GO; GO:0019866; C:inner membrane; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR004089; Chntaxis_transd.
DR InterPro; IPR003660; H1b_kin_HAMP.
DR Pfam; PF00672; HAMP; 1.
DR Pfam; PF00015; MCPsignal; 1.
DR SMART; SM00304; HAMP; 1.
DR SMART; SM00283; NA; 1.
DR PROSITE; PSS0111; CHEMOTAXIS_TRANSDUC_2; 1.
DR PROSITE; PSS0885; HAMP; 1.
KW Complete proteome.
SQ SEQUENCE 578 AA; 63178 MW; 55004ADC7356DA18 CRC64;

Query Match 63.6%; Score 42; DB 2; Length 578;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 3 WEIVGYFD 10
|||:|
Db 204 WEIVGYID 211

Search completed: December 4, 2005, 04:52:22
Job time : 102.375 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:45 ; Search time 15.5833 Seconds
(without alignments)
67.918 Million cell updates/sec

Title: US-10-632-706-128

Sequence: 1 GPWELVGYFDS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	68.2	279	2 T35791	probable transmem
2	44	65.7	367	2 AD0922	hypothetical prote
3	43	65.2	1788	2 T29043	glutamine synthet
4	41	62.1	491	2 E69368	hypothetical prote
5	41	62.1	550	2 B84900	glucokinase regula
6	41	62.1	619	1 S48729	hypothetical prote
7	41	62.1	697	2 G70704	ABC transporter ML
8	40	60.6	724	2 B87015	ABC-type transport
9	40	60.6	726	2 T44905	probable DNA-direc
10	40	60.6	868	2 D84824	probable plasma me
11	40	60.6	931	2 F84637	hypothetical prote
12	39	59.1	239	2 D71051	hypothetical prote
13	39	59.1	320	2 T33303	glutamate dehydrog
14	39	59.1	459	2 S17907	ribL-protein VC024
15	39	59.1	471	2 S28476	methyL-accepting c
16	39	59.1	578	2 B82204	H+-exporting ArpA
17	39	59.1	949	1 PXM0P1	NADH2 dehydrogenas
18	38	57.6	173	2 S44033	glutamate uptake fa
19	38	57.6	274	2 C75335	male protein homol
20	38	57.6	409	2 S63614	ankyrin repeat pro
21	38	57.6	432	2 T17829	hypothetical prote
22	38	57.6	465	2 T26146	apolipoprotein n-a
23	38	57.6	496	2 G97761	apolipoprotein N-a
24	38	57.6	499	2 AF3498	hypothetical prote
25	38	57.6	532	2 AF3498	hypothetical prote
26	38	57.6	1091	2 T34247	hypothetical prote
27	38	57.6	1107	2 T34246	probable polyacid
28	38	57.6	2100	2 T03223	hypothetical prote
29	37	56.1	213	2 C64041	hypothetical prote

30	37	56.1	217	2 A82491	fine protein VCA01
31	37	56.1	226	2 A87664	hypothetical prote
32	37	56.1	235	2 T44679	spu protein homol
33	37	56.1	241	2 T39330	probable 60S acid
34	37	56.1	276	2 A95309	probable ABC trans
35	37	56.1	277	2 AF3216	ABC transporter, m
36	37	56.1	349	2 T31855	hypothetical prote
37	37	56.1	365	2 S61636	hypothetical prote
38	37	56.1	400	2 AF0291	probable drug resi
39	37	56.1	413	2 G95965	conserved hypothet
40	37	56.1	426	2 T08550	choline monooxygen
41	37	56.1	462	2 T58179	5HT3 receptor subu
42	37	56.1	468	2 T48615	hypothetical prote
43	37	56.1	502	2 S50519	hypothetical prote
44	37	56.1	601	1 A64222	heat shock protein
45	37	56.1	642	2 G69371	acetyl-CoA synthe

ALIGNMENTS

RESULT 1
T35791
probable transmembrane sugar transport protein - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C/Accession: T35791
R/Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1998
A/Reference number: Z21570
A/Accession: T35791
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-279 <SEB>
A/Cross-references: UNIPROT:087858; UNIPARC:UPI0000ODACA7; EMBL:AL031013; PIDN:CAA19796
A/Experimental source: strain A3(2)
C/Genetics:
A/Genes: SC0EDB:SC8A6.24
C/Superfamily: maltose transport protein malG

Query Match
Best Local Similarity 77.8%; Score 45; DB 2; Length 279;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 WEVGYFDS 11
DB 160 WMLIGYFDS 168

RESULT 2
AD0922
probable undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase STY3637 [imported]
C/Species: Salmonella enterica subsp. enterica serovar Typhi
A/Note: this species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 03-Feb-2003
C/Accession: AD0922
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero-
A/Reference number: AB0502; WUID:21534947; PMID:11677608
A/Accession: AD0922
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-367 <PAR>
A/Cross-references: UNIPARC:UPI000005A56F; GB:AL513382; PIDN:CAD09398.1; PID:G16504516;
C/Genetics:
A/Genes: STY3637

Query Match
Best Local Similarity 69.2%; Score 44; DB 2; Length 367;
Pred. No. 5.6;

```
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
Qy 1 GPMELVY---GYF 9
Db 127 GPMELVLPGRGFF 139

RESULT 3
729043
hypothetical protein B0228.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T29043
R:Leimbach, D.
submitted to the EMBL Data Library, March 1995
A:Description: The sequence of C. elegans cosmid B0228.
A:Reference number: Z18324
A:Accession: T29043
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1788 <LEI>
A:Cross-references: UNIPROT:Q81G61, UNIPARC:UPI00000851C9, EMBL:U23168, PIDN:AA038806.1,
A:Experimental source: strain Bristol N2
A:Gene: CESP:B0228.2
A:Introns: 1456/2; 1482/3; 1516/2; 1551/3; 1595/3; 1646/1; 1671/1; 1716/2; 1749/3

Query Match
Best Local Similarity 65.2%; Score 43; DB 2; Length 1788;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPMELVGYFD 10
Db 1722 GPMNMGRFD 1731

RESULT 4
B69368
glutamine synthetase (glnA) homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: B69368
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirschner, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Goeyne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Usterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: B69368
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-491 <KLE>
A:Cross-references: UNIPROT:Q29313; UNIPARC:UPI0000056F0D; GB:AE001039; GB:AE000782; NID
C:Superfamily: glutamate-aminonia ligase

Query Match
Best Local Similarity 62.1%; Score 41; DB 2; Length 491;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PWELVGYFD 10
Db 482 PWEFMKTFD 490

RESULT 5
B84900
hypothetical protein At2g46220 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: B84900
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
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M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umeyam, L.; Tallon, L.;
ues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: B84900
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-550 <STO>
A:Cross-references: UNIPROT:O82347, UNIPARC:UPI000017A71B, GB:AE002093; NID:G370227, PIR
C:Gene: At2g46220
A:Map position: 2

Query Match
Best Local Similarity 62.1%; Score 41; DB 2; Length 550;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPMELVGYFD 10
Db 176 GPMETRGKFD 185

RESULT 6
S48729
glucokinase regulator - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S48729; S49339
R:Veiga-da-cunha, M.; Decheux, M.; Motelet, N.; van Schaftingen, B.
Eur. J. Biochem. 225, 43-51, 1994
A:Title: Cloning and expression of a Xenopus liver cDNA encoding a fructose-phosphate-in
A:Reference number: S48729; MUID:95010134; PMID:7925465
A:Accession: S48729
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-619 <VEI>
A:Cross-references: UNIPROT:Q91754; UNIPARC:UPI000012B2E2; EMBL:X80901; NID:G556677; PIDN
C:Superfamily: glucokinase regulator

Query Match
Best Local Similarity 62.1%; Score 41; DB 1; Length 619;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPMELVGYFDS 11
Db 17 GPMELVGYEES 27

RESULT 7
G70704
hypothetical protein RV2326c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: G70704
R:Coile, S.T.; Broese, R.; Parbhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: G70704
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-697 <COL>
A:Cross-references: UNIPROT:P71886; UNIPARC:UPI000013BA74; GB:Z79702; GB:AL123456; NID:G3
C:Experimental source: strain H37RV
A:Gene: RV2326c

Query Match
Best Local Similarity 62.1%; Score 41; DB 2; Length 697;
```

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PMELVGYFD 10
|||:||||
DB 196 PMVLGGYFN 204

RESULT 8

B87015

ABC transporter ML0848 [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C:Accession: B87015

R:Coile, S.T.; Elzmeier, K.; Parhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho

R.; Davis, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

eem, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A:Author: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq

A:Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; PMID:11234002

A:Accession: B87015

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-724 <STO>

A:Cross-references: UNIPROT:Q9CF9; UNIPARC:UPI00000C6D27; GB:AL450380; NID:G13092926; F

C:Genetics:

A:Gene: ML0848

Query Match 60.6%; Score 40; DB 2; Length 724;
Best Local Similarity 75.0%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PMELVGYF 9
|||:||||
DB 224 PMVLGGYFN 231

RESULT 9

T44905

ABC-type transporter homolog [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004

C:Accession: T44905

R:Parhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1997

A:Reference number: Z22864

A:Accession: T44905

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-726 <PAR>

A:Cross-references: UNIPROT:Q32971; UNIPARC:UPI00000BBD0E; EMBL:Z98741; PIDN:CAB11403.1

C:Genetics:

A:Experimental source: cosmid B22

A:Note: MLCB22.38c

Query Match 60.6%; Score 40; DB 2; Length 726;
Best Local Similarity 75.0%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PMELVGYF 9
|||:||||
DB 226 PMVLGGYFN 233

RESULT 10

D84824

probable DNA-directed RNA polymerase II subunit [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: D84824

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; PMID:20083487; PMID:10617197

A:Accession: D84824

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-888 <STO>

A:Cross-references: UNIPROT:O04206; UNIPARC:UPI00000A517F; GB:AE002093; NID:G2088656; PI

A:Genetics:

A:Gene: At2g40030

A:Map position: 2

Query Match 60.6%; Score 40; DB 2; Length 888;
Best Local Similarity 63.6%; Pred. No. 70;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPMELVGYFDS 11
|||:||||
DB 544 GPKETLGFDS 554

RESULT 11

F84637

probable plasma membrane proton ATPase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004

C:Accession: F84637

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; PMID:20083487; PMID:10617197

A:Accession: F84637

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-931 <STO>

A:Cross-references: UNIPARC:UPI000016237B; GB:AE002093; NID:G4572678; PIDN:AAD23893.1; G

C:Genetics:

A:Gene: At2g24520

A:Map position: 2

C:Superfamily: Na(+)/K(+)-transporting ATPase alpha chain; ATPase nucleotide-binding dom

Query Match 60.6%; Score 40; DB 2; Length 931;
Best Local Similarity 85.7%; Pred. No. 74;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPMELVYG 7
|||:||||
DB 457 GPMQLVYG 463

RESULT 12

D71051

hypothetical protein PH1107 - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 31-Dec-2004

C:Accession: D71051

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hatakeyama, Y.; Hino, Y.; Yamamoto, S.; Sekin

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kuehida, N.; Oguchi

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a

A:Reference number: A71000; PMID:98344137; PMID:9679194

A:Accession: D71051

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-239 <KAW>

A:Cross-references: UNIPROT:O58834; UNIPARC:UPI0000062FB7; GB:AP000005; NID:G3236132; PI

A:Experimental source: strain 073

A:Note: this accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics:

A:Gene: PH1107

C:Superfamily: glycosidase, PH1107 type

Query Match 59.1%; Score 39; DB 2; Length 299;
 Best Local Similarity 60.0%; Pred. No. 33;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PMELVGYFDS 11
 |||||
 Db 247 PMELGHDVN 256

RESULT 13

T33303
 hypothetical protein R01B10.4 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C:Accession: T33303
 R:Langston, Y.; Beck, C.
 Submitted to the EMBL Data Library, May 1998

A:Description: The sequence of *C. elegans* cosmid R01B10.

A:Reference number: 221318

A:Accession: T33303

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-320 <LAN>

A:Cross-references: UNIPROT:O61975; UNIPARC:UPI0000080228; EMBL:AF068718; PIDN:AC17768.

A:Experimental source: strain Bristol N2; clone R01B10

C:Genetics:

A:Gene: CESP:R01B10.4

A:Map position: 5

A:Introns: 25/2; 73/2; 211/3; 241/2

Query Match 59.1%; Score 39; DB 2; Length 320;
 Best Local Similarity 55.6%; Pred. No. 36;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 MELVGYFDS 11
 |||||
 Db 65 WDIGHFDS 73

RESULT 14

S17907
 glutamate dehydrogenase (NADP) (EC 1.4.1.4) - yeast (*Schwanniomyces occidentalis* var. *oc*

C:Species: *Schwanniomyces occidentalis* var. *oc*

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 05-Oct-2004

C:Accession: S17907

R:de Zeyva, P.A.; Connerton, I.F.; Watson, D.C.; Johnston, J.R.

Curr. Genet. 20, 219-224, 1991

A:Title: Cloning, sequencing and expression of the *Schwanniomyces occidentalis* NADP-depe

A:Reference number: S17907; MUID:92035089; PMID:1934128

A:Accession: S17907

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-459 <DEZ>

A:Cross-references: UNIPROT:P29507; UNIPARC:UPI00001292P9

C:Superfamily: glutamate dehydrogenase

C:Keywords: NADP; oxidoreductase

Query Match 59.1%; Score 39; DB 2; Length 459;
 Best Local Similarity 66.7%; Pred. No. 52;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PMELVGYFD 10
 |||||
 Db 308 PMAKVGHFD 316

RESULT 15

S28476

rfbL protein VCO249 [similarity] - *Vibrio cholerae* (strain N16961 serogroup O1)

C:Species: *Vibrio cholerae*

C:Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004

C:Accession: S28476; H82346

R:Manning, P.A.
 submitted to the EMBL Data Library, May 1991

A:Reference number: S28467

A:Accession: S28476

A:Molecule type: DNA

A:Residues: 1-471 <MAN>

A:Cross-references: UNIPROT:O06959; UNIPARC:UPI00000D470B; EMBL:X59554; NID:G48381; PIDN:

A:Experimental source: strain 017

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;

Chardson, D.; Brimolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, P

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: H82346

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-471 <HEI>

A:Cross-references: UNIPARC:UPI00000D470B; GB:AE004113; GB:AE003852; NID:99654648; PIDN:

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: rfbL; VCO249

A:Map position: 1

C:Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology

F/47-468/Domain: acetate-CoA ligase homology <ACI>

Query Match 59.1%; Score 39; DB 2; Length 471;
 Best Local Similarity 60.0%; Pred. No. 54;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PMELVGYFDS 11
 |||||
 Db 329 PMMLDGYFN 338

Search completed: December 4, 2005, 04:53:34
 Job time: 17.5833 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:09:54 ; Search time 95.5625 Seconds
(without alignments).
50.576 Million cell updates/sec

Title: US-10-632-706-128
Perfect score: 66
Sequence: 1 GPMELVGFYDS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq 21:*

- 1: geneeqp1980s:*
- 2: geneeqp1990s:*
- 3: geneeqp2000s:*
- 4: geneeqp2001s:*
- 5: geneeqp2002s:*
- 6: geneeqp2003as:*
- 7: geneeqp2003bs:*
- 8: geneeqp2004s:*
- 9: geneeqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	11	8	ADR38726
2	44	66.7	306	6	ABU45531 Protein e
3	44	66.7	367	6	ABU47042 Protein e
4	44	66.7	367	6	ABU47877 Protein e
5	43	65.2	207	8	ADH12894
6	42	63.6	415	7	ABM89126 Rice abio
7	41	62.1	114	4	AAO08773 Human pol
8	41	62.1	121	2	AAH88504 Vhm for
9	41	62.1	475	6	ABU20453 Protein e
10	41	62.1	792	7	ADC07986 Rice prot
11	41	62.1	1352	4	ABM67542 Drosophila
12	40	60.6	146	6	ABP56656 Chimpanze
13	40	60.6	283	6	ABM70292 Phototrab
14	40	60.6	477	8	ADY22314 Plant ful
15	40	60.6	885	3	AAG32050 Arabidops
16	40	60.6	931	3	AAG32049 Arabidops
17	40	60.6	956	3	AAG32048 Arabidops
18	39.5	59.8	511	8	ADR89844 Plant ful
19	39	59.1	79	3	AAH3353 Arabidops
20	39	59.1	103	3	AAH3353 Arabidops
21	39	59.1	112	4	AAH3351 Arabidops
22	39	59.1	166	4	AAH06860 Human foe
23	39	59.1	211	8	ADM57065 A thalian
24	39	59.1	233	3	AAH05440 Arabidops

25	39	59.1	233	3	AAH38801	AAH38801 Arabidops
26	39	59.1	242	5	ABG69053	ABG69053 Amino aci
27	39	59.1	254	3	AAH30761	AAH30761 Arabidops
28	39	59.1	257	3	AAH38800	AAH38800 Arabidops
29	39	59.1	257	3	AAH05439	AAH05439 Arabidops
30	39	59.1	266	3	AAH05438	AAH05438 Arabidops
31	39	59.1	266	3	AAH38799	AAH38799 Arabidops
32	39	59.1	266	5	ABH92172	ABH92172 Herbicida
33	39	59.1	274	9	ABM95054	ABM95054 M. xanthu
34	39	59.1	278	3	AAH30760	AAH30760 Arabidops
35	39	59.1	287	3	AAH30759	AAH30759 Arabidops
36	39	59.1	537	8	ADT60469	ADT60469 Plant pol
37	39	59.1	670	6	ABU18890	ABU18890 Protein e
38	39	59.1	696	4	ABG20404	ABG20404 Novel hum
39	39	59.1	775	4	AAU48754	AAU48754 Propionib
40	39	59.1	775	6	ABM65954	ABM65954 Propionib
41	39	59.1	775	6	ABM45273	ABM45273 Propionib
42	39	59.1	877	3	AAH36913	AAH36913 Arabidops
43	39	59.1	885	3	AAH36912	AAH36912 Arabidops
44	39	59.1	949	3	AAH36911	AAH36911 Arabidops
45	38	57.6	48	4	AAH95055	AAH95055 Human rep

ALIGNMENTS

RESULT 1
ADR38726 standard; peptide, 11 AA.

ADR38726;
02-DEC-2004 (first entry)

Mouse heavy chain variable region CDR3 seqid 128.

antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KMW toxin neutralisation; botulinum neurotoxin poisoning; mouse;
KMW heavy chain variable region; complementarily determining region; CDR3.

Mus sp.
US2004175385-A1.

09-SEP-2004.

01-AUG-2003; 2003US-00632706.

31-AUG-1998; 98US-00144886.
01-AUG-2002; 2002US-0400721P.

(REGC) UNIV CALIFORNIA.

Marks JD, Amerdorfer P;
WPI; 2004-652009/63.

New isolated antibody that neutralizes botulinum neurotoxin type A,
useful for diagnosing botulism or for treating pathologies associated
with botulinum neurotoxin poisoning.

Example 3; SEQ ID NO 128; 110pp; English.

The invention describes an isolated antibody (I) that specifically binds
to an epitope specifically bound by an antibody expressed by a specific
clone where (I) binds to and neutralizes botulinum neurotoxin type A
(BoNT/A). An isolated antibody (II) that specifically binds to an epitope
specifically bound by an antibody expressed by a clone chosen from clone
S25, C39, 106, 3D12, B4, 1F3, huc25, Ar1, Ar2, WRI (V), WRI (F), 3-1,
3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
comprising BoNT/A neutralising epitope having an epitope that is

CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC producing (1); and a composition (III) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC BONT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulinum
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BONT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain variable region complementarity determining
CC region 3 (CD3) from anti-botulinum neurotoxin antibodies.
XX
SQ Sequence 11 AA;
Query Match 100.0%; Score 66; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPMELVGYFDS 11
Db 1 GPMELVGYFDS 11
RESULT 2
ABU45531
ID ABU45531 standard; protein; 306 AA.
XX
AC ABU45531;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #31058.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Salmomella paratyphi.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JM;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
XX
DR N-PSDB; ACA49401.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 73455; 1766bp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 623 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC from [ftp://www.int/pub/published_pcr_sequences](http://www.int/pub/published_pcr_sequences)
XX
SQ Sequence 306 AA;
Query Match 66.7%; Score 44; DB 6; Length 306;
Best Local Similarity 69.2%; Pred. No. 40;
Matches 9; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 1 GPMELV-----GYF 9
Db 66 GPMELVAGPFGYF 78
RESULT 3
ABU47042
ID ABU47042 standard; protein; 367 AA.
XX
AC ABU47042;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #32569.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Salmomella typhimurium.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JM;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
XX
DR N-PSDB; ACA50912.


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XX XX WO2004003009-A2.
XX PN
XX PD 08-JAN-2004.
XX PF 26-JUN-2003; 2003WO-GB002718.
XX PR 28-JUN-2002; 2002GB-00014942.
XX PA (MINA ) UK SEC FOR DEFENCE.
XX PI Titball RW, Mayers CN, Duffield ML, Miller J, Rowe SC;
XX DR N-PDB; ADH12994.
XX PF MPI; 2004-083016/08.
XX PT New protein, useful as a vaccine for producing a protective immune
XX PR response in a mammal against infection by Francisella tularensis, or
XX PT preventing or treating Francisella tularensis infection in a mammal.
XX PS Claim 1; SEQ ID NO 75; 217pp; English.
XX CC The invention relates to 100 potentially immunogenic proteins from
XX CC Francisella tularensis (ADH12820-ADH12919) and nucleic acids encoding
XX CC them (ADH12920-ADH13019) which may be used in vaccines. The nucleic acids
XX CC may be contained within a vaccine, bacterial or plasmid vector. The
XX CC invention also relates to a pharmaceutical composition comprising the
XX CC protein or the nucleic acid in combination with a pharmaceutical carrier
XX CC or excipient. The proteins and nucleic acids are useful in vaccine
XX CC compositions for producing a protective immune response against
XX CC Francisella tularensis infection in a mammal, or for preventing or
XX CC treating Francisella tularensis infection in a mammal. The present
XX CC sequence represents a Francisella tularensis protein of the invention.
XX SQ Sequence 207 AA;
XX
XX Query Match 65.2%; Score 43; DB 8; Length 207;
XX Best Local Similarity 100.0%; Pred. No. 39;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GPMELVVG 7
XX |||||
XX DB 120 GPMELVVG 126
XX
XX RESULT 6
XX ID ABBM89126 standard; protein; 415 AA.
XX AC ABBM89126;
XX DT 02-JUN-2005 (first entry)
XX DE Rice abiotic stress responsive polypeptide SEQ ID NO:7372.
XX KM abiotic stress tolerance; transgenic plant; cereal; agriculture.
XX OS Oryza sativa.
XX PN MO2003008540-A2.
XX PD 30-JAN-2003.
XX PF 21-JUN-2002; 2002WO-US019668.
XX PR 22-JUN-2001; 2001US-0300112P.
XX PR 24-AUG-2001; 2001US-0314662P.
XX PR 26-SEP-2001; 2001US-0325277P.
XX PR 21-NOV-2001; 2001US-0332132P.
XX PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX PI Kreps J, Briggs SP, Cooper B, Glaesbrook J, Goff SA, Katagiri F;

```

PI	Moughamer T, Provart N, Ricke D, Zhu T;
XX	
DR	WPI; 2003-248011/24.
XX	
XX	New stress-responsive nucleic acid, useful for altering the
PT	responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT	stress, salt stress or osmotic stress.
PT	
XX	
PS	Claim 1; SEQ ID NO 7372; 89pp, English.
XX	
CC	The invention relates to novel abiotic stress responsive polynucleotides
CC	and polypeptides. Also disclosed are vectors, expression cassettes, host
CC	cells, and plants containing such polynucleotides. Also disclosed are
CC	methods for using the polynucleotides and polypeptides to alter the
CC	responsiveness of a plant to abiotic stress. The invention is useful in
CC	agriculture. The nucleic acid is useful for determining whether a test
CC	plant has been exposed to an abiotic stress condition. It is also useful
CC	for selecting an agent that alters abiotic stress regulated
CC	polynucleotide expression in a plant cell, and to identify a homolog or
CC	ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC	responsible and the polypeptide encoded by it are useful in altering the
CC	responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC	stress, osmotic stress or any of their combinations. The present sequence
CC	is used in the exemplification of the invention
XX	
XX	Sequence 415 AA;
XX	
Query Match	63.6%; Score 42; DB 7; Length 415;
Best Local Similarity	75.0%; Pred. No. 1.2e+02;
Matches	6; Conservative 1; Mismatches 1; Indels 0; Gaps 0
Oy	1 GPMELVGY 8
	:
Db	176 GPMELTGF 183
XX	
RESULT 7	
AA008773	
ID	AA008773 standard; protein; 114 AA.
XX	
AC	AA008773;
XX	
DT	06-NOV-2001 (first entry)
XX	
DE	Human polypeptide SBQ ID NO 22665.
XX	
KW	Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW	tissue growth factor; immunomodulatory; cancer; leukemia;
KW	nervous system disorders; arthritis; inflammation.
XX	
OS	Homo sapiens.
XX	
PN	WO200164835-A2.
XX	
PD	07-SEP-2001.
XX	
PF	26-FEB-2001; 2001WO-US004927.
XX	
PR	28-FEB-2000; 2000US-00515126.
PR	18-MAY-2000; 2000US-00577409.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Tang YT, Liu C, Drmanac RT;
XX	
DR	WPI; 2001-514838/56.
DR	N-PSDB; AAI88704.
XX	
PT	Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT	and treating e.g. leukemia, inflammation and immune disorders.
XX	
PS	Claim 20; SEQ ID NO 22665; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AA000010-AA013910) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activating/inhibiting activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 114 AA;

Query Match 62.1%; Score 41; DB 4; Length 114;
Best Local Similarity 55.6%; Pred. No. 46;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVGYF 9
| | | | | | | | | |
Db 76 GPMKFLGFF 84

RESULT 8

ID AAR88504 standard; protein; 121 AA.

AAR88504;

31-JUL-1996 (first entry)

VHmu for antibody BT34/A5.

Antibody; variable heavy chain; VHmu; human; monoclonal; Mab; BT34/A5;

BT32/A6; cell cycle independent; tumour specific; glioma; therapy;

detection; complementarity determining region; CDR.

Homo sapiens.

Location/Qualifiers

Key 31.35
Region /note="complementarity determining region (specifically
claimed)"Region 50.66
/note="complementarity determining region (specifically
claimed)"Region 99.110
/note="complementarity determining region (specifically
claimed)"

Region

WO953374-A1.

28-DEC-1995.

16-JUN-1995; 95MO-CA000361.

21-JUN-1994; 94US-00264093.

(DANM/) DAN M D.

Dan MD;

WPI, 1996-058411/06.

N-PSDB; AAT10938.

Novel monoclonal antibodies, BT34/A5 and BT32/A6 - used to characterise

glioma specific cell surface antigens, and in the treatment of glioma.

Claim 8, Page 33, 53pp; English.

CC AAR88504-R88510 represent regions of the human monoclonal antibodies
CC (Mab's) BT34/A5 and BT32/A6. This sequence represents the variable region
CC of the heavy chain, subgroup mu, (VHmu) of BT34/A5. The complementarity
CC determining regions (CDR's) of this sequence are specifically claimed.
CC This sequence preferably has an N-terminal extension comprising the
CC signal sequence represented in AAR88505. The BT34/A5 and BT32/A6 Mab's
CC recognise a cell cycle independent tumour specific antigen. They also
CC bind equally well to tumour cells in vitro regardless of their culture
CC viability, growth characteristics, or culture density. The antibodies
CC effectively label the tumour cells by binding to the antigen present on
CC the cell surface. The Mab's are useful in the detection and the treatment
CC of glioma. These Mab's are specific for glioma and show none of the cross
CC reactivity seen with previous antibodies
XX

SQ Sequence 121 AA;

Query Match 62.1%; Score 41; DB 2; Length 121;
Best Local Similarity 60.0%; Pred. No. 49;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPMELVGYFD 10
| | | | | | | | | |
Db 100 GYMDLNLVYFD 109

RESULT 9

ID ABU20453 standard; protein; 475 AA.

ABU20453;

19-JUN-2003 (first entry)

Protein encoded by prokaryotic essential gene #5980.

Antisense; prokaryotic essential gene; cell proliferation; drug design.

Bacteroides fragilis.

WO20027183-A2.

03-OCT-2002.

21-MAR-2002; 2002MO-US009107.

21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-OCT-2001; 2001US-0342823P.

08-FEB-2002; 2002US-00072851.

06-MAR-2002; 2002US-0362699P.

(ELIT-) ELITRA PHARM INC.

Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KU, Zyckind JW,

Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;

WPI; 2003-029926/02.

N-PSDB; ACA24323.

Claim 25, SEQ ID NO 48377; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins (AB857737-
 CC AB872072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

SO Sequence 1352 AA;

Query Match 62.1%; Score 41; DB 4; Length 1352;

Best Local Similarity 77.8%; Pred. No. 6.3e+02;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 MELVGFDS 11

DB 161 WRNMGVFD 169

RESULT 12

ABP56656 standard; protein; 146 AA.

AC ABP56656;

DT 25-MAR-2003 (first entry)

DE Chimpanzee C68 adenovirus E3 16 kDa protein SEQ ID NO:21.

XX Chimpanzee C68 adenovirus; rapid screening; bacterial transformant;

KW simian adenovirus; cytosolic; antiproliferative; antitumor; vaccine;

KW adenoviral capsid protein; hexon; penton; fibre protein; cancer;

KW hyperplastic condition; psoriasis; infection.

XX Mastadenovirus.

XX Key Location/Qualifiers

FT Misc-difference 62 /note="any amino acid"

XX WO200300851-A2.

XX 03-JAN-2003.

XX 20-JUN-2002; 2002WO-US019735.

XX 22-JUN-2001; 2001US-0300501P.

XX 04-JUN-2002; 2002US-0385632P.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Gao G, Wilson JM;

XX MPI: 2003-184043/18.

XX N-PSDB; AB222473.

XX New C68 chimpanzee adenoviral capsid protein, useful for preparing a

XX composition for treating hyperproliferative conditions e.g., cancer or

XX psoriasis and as a vaccine against bacterial, fungal, viral or parasitic

XX infection.

XX Disclosure; Page 88; 124pp; English.

XX The present invention describes a chimpanzee C68 adenoviral capsid

XX protein, which is substantially free of other viral proteins with which

XX it is naturally associated, comprising: (a) a hexon protein comprising

XX 513-amino acid sequence (see ABP56652); (b) a penton protein comprising

XX 534-amino acid sequence (see ABP56647); (c) a fibre protein comprising

XX 425-amino acid sequence (see ABP56652); or (d) a unique fragment of any

XX of (A)-(C) comprising 8-amino acid residues in length. Also described:

XX (1) a novel adenovirus serotype comprising a unique fragment of the C68

XX hexon protein fused to a heterologous adenovirus hexon peptide; (2) a

XX recombinant or pseudocapsid adenovirus comprising a capsid of the novel

XX adenovirus serotype encapsidating a molecule for delivery to a target

XX cell; (3) an adenoviral capsid; (4) a pharmaceutical composition; (5)

CC rapid screening of recombinant constructs; and (6) a host cell. The

CC chimpanzee C68 adenoviral capsid protein has cytostatic, antiproliferative

CC and antimicrobial activities, and can be used in vaccines. The chimpanzee

CC C68 adenoviral capsid protein is useful for preparing a composition for

CC treating hyperproliferative conditions e.g., cancer or psoriasis and as a

CC vaccine against bacterial, fungal, viral or parasitic infection. The

CC present sequence represents a chimpanzee C68 adenovirus E3 16 kDa

CC protein, which is given in the exemplification of the present invention

SO Sequence 146 AA;

Query Match 60.6%; Score 40; DB 6; Length 146;

Best Local Similarity 85.7%; Pred. No. 89;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPMELVVG 7

DB 101 GPMELVVG 107

RESULT 13

ABM70292 standard; protein; 283 AA.

AC ABM70292;

DT 20-NOV-2003 (first entry)

DE Photorhabdus luminescens protein sequence #3389.

XX Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;

XX detection; food; gene expression; plant; animal; microorganism; toxin;

XX antibiotic; biopesticide; virulence factor; disease model; plague;

XX whooping cough.

XX Photorhabdus luminescens.

XX WO200294867-A2.

XX 28-NOV-2002.

XX 07-FEB-2002; 2002WO-IB003040.

XX 07-FEB-2001; 2001FR-00001659.

XX (INSP) INST PASTEUR.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst P, Danchin A;

XX Buchrieser C;

XX MPI: 2003-148459/14.

XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,

XX useful e.g. as therapeutic antimicrobials and agricultural pesticides.

XX Claim 2; SEQ ID NO 3389; 1205pp; French.

XX The invention relates to the isolation of genes and their encoded

XX proteins from Photorhabdus luminescens. The isolated sequences are

XX sources of probes and primers for detecting the genome of P. luminescens

XX and related species; to study polymorphisms; for gene analysis and for

XX detection/amplification of the genes. Antibodies (Ab) raised against the

XX of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that

XX carry a gene-containing vector are used to select compounds that

XX modulate, regulate, induce or inhibit expression of the genes in plants,

XX animals or microorganisms other than P. luminescens and are able to alter

XX response or sensitivity to toxins and antibiotics produced by P.

XX luminescens. Cells transformed to express the genes are useful for

XX recombinant production of the proteins, particularly toxins and

XX antibacterials useful as insecticides, bactericides and fungicides. The

XX genes, proteins, vectors containing the genes and Ab are also useful

CC therapeutically (to treat microbial infection by bacteria or fungi that
CC are sensitive to *P. luminescens*-encoded toxins or antibiotics) and as
CC biopesticides. Other uses of the genes and the proteins are as virulence
CC factors and for identifying targets of human diseases for which *P.*
CC *luminescens* is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated *P. luminescens* proteins
XX
SQ Sequence 283 AA;
Query Match 60.6%; Score 40; DB 6; Length 283;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 3 MELVGFDS 11
DB 238 MELVGFDA 246
RESULT 14
ID ADY22314 standard; protein; 477 AA.
XX ADY22314;
XX 21-APR-2005 (first entry)
XX
XX Plant full length insert polypeptide seqid 70098.
XX
XX plant protectant; plant growth regulant; gene therapy; plant;
XX recombinant DNA construct; physical array; plant breeding marker;
XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX extreme osmotic condition; pathogen tolerance; pest tolerance;
XX growth rate; cell cycle pathway; disease resistance;
XX galactomannan production; lignin production; plant growth regulator;
XX yield; plant growth; plant development; seed oil; protein yield;
XX
XX
XX Undifferentiated.
XX
XX US2004034888-A1.
XX
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
XX
XX 05-NOV-2001; 2001US-00985678.
XX
XX (LIUJ/) LIU J.
XX (ZHOU/) ZHOU Y.
XX (KOVA/) KOVALIC D K.
XX (SCRE/) SCREEN S E.
XX (TABAS/) TABASKA J E.
XX (CAOY/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
XX MPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX pests, for conferring increased resistance to plant disease, or for
XX improving yield.
XX
XX Claim 1; SEQ ID NO 70098; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
XX of the invention are also useful in physical arrays of molecules and as
XX plant breeding markers. The recombinant DNA construct is useful for
XX improving plant tolerance to cold, heat, drought, herbicides, extreme

CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This is the amino acid sequence of a plant full length insert
CC polypeptide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 477 AA;
Query Match 60.6%; Score 40; DB 8; Length 477;
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 GPMELVGFDFD 10
DB 307 GPMELVGFDFD 316
RESULT 15
ID AAG32050 standard; protein; 885 AA.
XX AAG32050;
XX 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 38593.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
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XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
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XX 25-FEB-1999; 99US-0121825P.
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XX 29-MAR-1999; 99US-0126785P.
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XX 01-APR-1999; 99US-0127462P.
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PR 11-AUG-1999; 99US-0148319P.
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PR 13-AUG-1999; 99US-0148565P.
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PR 17-AUG-1999; 99US-0149175P.
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 PR 29-OCT-1999; 99US-0162142P.

Query Match 60.6%; Score 40; DB 3; Length 885;
 Best Local Similarity 85.7%; Pred. No. 6e+02; 0; Indels 0; Gaps 0;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPMQLVG 7
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 Db 411 GPMQLVG 417

Search completed: December 4, 2005, 04:44:57
 Job time : 98.5625 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 4, 2005, 04:08:08, Search time 3.20833 Seconds
(without alignments)
16.417 Million cell updates/sec

Title: US-10-632-706-128
Perfect score: 66
Sequence: 1 GPWELVGYFDS 11

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications_AA_New.*
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4: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	54.5	792	6	US-10-467-657-6026
2	36	54.5	792	6	US-10-467-657-7528
3	35	53.0	356	6	US-10-467-657-1210
4	34	51.5	322	7	US-11-074-176-36
5	34	51.5	723	6	US-10-467-657-1916
6	34	51.5	926	6	US-10-841-129-2
7	33.5	50.8	478	7	US-11-037-829A-4
8	33	50.0	198	7	US-11-082-389-302
9	33	50.0	281	7	US-11-082-389-304
10	33	50.0	431	7	US-11-055-822-76
11	33	50.0	724	6	US-10-131-826A-60
12	33	50.0	1510	6	US-11-055-822-72
13	33	50.0	2725	7	US-11-113-424-52
14	32	48.5	456	6	US-10-467-657-4150
15	32	48.5	533	7	US-11-147-047-33
16	32	48.5	771	7	US-11-147-047-34
17	31.5	47.7	532	7	US-11-184-380-6
18	31.5	47.7	534	6	US-10-719-311-18
19	31.5	47.7	584	6	US-11-184-380-5
20	31.5	47.7	598	6	US-10-719-311-16
21	31.5	47.7	724	7	US-11-184-380-4
22	31.5	47.7	734	6	US-10-719-311-4
23	31.5	47.7	735	7	US-11-184-380-24
24	31	47.0	142	6	US-10-821-234-1030
25	31	47.0	229	6	US-10-510-386-228

26	31	47.0	290	6	US-10-793-626-214	Sequence 214, App
27	31	47.0	393	6	US-10-821-234-1292	Sequence 1292, App
28	31	47.0	490	6	US-10-131-826A-310	Sequence 310, App
29	31	47.0	626	6	US-10-467-657-6426	Sequence 6426, App
30	31	47.0	626	6	US-10-467-657-7618	Sequence 7618, App
31	31	47.0	745	7	US-11-109-156-14	Sequence 14, App
32	31	47.0	766	6	US-10-522-789-2	Sequence 2, App
33	30	45.5	31	6	US-10-467-657-2188	Sequence 2188, App
34	30	45.5	180	6	US-10-665-455-11	Sequence 11, App
35	30	45.5	221	7	US-11-055-822-82	Sequence 82, App
36	30	45.5	389	6	US-10-979-821-2	Sequence 2, App
37	30	45.5	400	6	US-10-793-626-3116	Sequence 3116, App
38	30	45.5	450	6	US-10-467-657-2126	Sequence 2126, App
39	30	45.5	457	7	US-11-055-822-80	Sequence 80, App
40	30	45.5	479	6	US-10-821-234-871	Sequence 871, App
41	30	45.5	934	6	US-10-858-730-8	Sequence 8, App
42	30	45.5	1857	7	US-11-102-217-2	Sequence 2, App
43	29.5	44.7	17	6	US-10-939-890-116	Sequence 116, App
44	29.5	44.7	178	6	US-10-508-263-32	Sequence 32, App
45	29.5	44.7	178	6	US-10-508-263-46	Sequence 46, App

ALIGNMENTS

RESULT 1
US-10-467-657-6026
Sequence 6026, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqMan99, version 1.04
SEQ ID NO 6026
LENGTH: 792
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6026

Query Match 54.5%, Score 36, DB 6, Length 792;
Best Local Similarity 75.0%, Pred. No. 27;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 ELVGYFDS 11
DB 390 ELVGYFDN 397

RESULT 2
US-10-467-657-7528
Sequence 7528, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8

/ PRIOR FILING DATE: 2001-02-12
 / NUMBER OF SEQ ID NOS: 9218
 / SOFTWARE: SeqMin99, version 1.04
 / SEQ ID NO 7528
 / LENGTH: 792
 / TYPE: PRT
 / ORGANISM: Neisseria gonorrhoeae
 / US-10-467-657-7528

Query Match 54.5%; Score 36; DB 6; Length 792;
 Best Local Similarity 75.0%; Pred. No. 27;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 ELVGYFDS 11
 DB 390 ELVGYFDN 397

RESULT 3
 / US-10-467-657-1210
 / Sequence 1210, Application US/10467657
 / Publication No. US20050260581A1
 / GENERAL INFORMATION:
 / APPLICANT: CHIRON SPA
 / APPLICANT: FONTANA Maria Rita
 / APPLICANT: PIZZA Mariagrazia
 / APPLICANT: MASIGNANI Vega
 / APPLICANT: MONACI Elisabetta
 / TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 / FILE REFERENCE:
 / CURRENT APPLICATION NUMBER: US/10/467,657
 / CURRENT FILING DATE: 2003-08-11
 / PRIOR APPLICATION NUMBER: GB-0103424.8
 / PRIOR FILING DATE: 2001-02-12
 / NUMBER OF SEQ ID NOS: 9218
 / SOFTWARE: SeqMin99, version 1.04
 / SEQ ID NO 1210
 / LENGTH: 356
 / TYPE: PRT
 / ORGANISM: Neisseria gonorrhoeae
 / US-10-467-657-1210

Query Match 53.0%; Score 35; DB 6; Length 356;
 Best Local Similarity 62.5%; Pred. No. 19;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPMELVGY 8
 DB 45 GIMELVGY 52

RESULT 4
 / US-11-074-176-36
 / Sequence 36, Application US/11074176
 / Publication No. US20050250135A1
 / GENERAL INFORMATION:
 / APPLICANT: Kleenhammer, Todd R.
 / APPLICANT: Russell, William M.
 / APPLICANT: Altermann, Eric
 / APPLICANT: McAniff, Olivia
 / APPLICANT: Perill, Andrea Azcarate
 / TITLE OF INVENTION: Nucleic Acid Sequences Encoding
 / FILE REFERENCE: 5051-694
 / CURRENT APPLICATION NUMBER: US/11/074,176
 / CURRENT FILING DATE: 2003-03-07
 / PRIOR APPLICATION NUMBER: 60/551,161
 / PRIOR FILING DATE: 2004-03-08
 / NUMBER OF SEQ ID NOS: 381
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 36
 / LENGTH: 322
 / TYPE: PRT

/ ORGANISM: Lactobacillus acidophilus
 / US-11-074-176-36

Query Match 51.5%; Score 34; DB 7; Length 322;
 Best Local Similarity 85.7%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ELVGYFD 10
 DB 43 ELVGYFD 49

RESULT 5
 / US-10-467-657-1916
 / Sequence 1916, Application US/10467657
 / Publication No. US20050260581A1
 / GENERAL INFORMATION:
 / APPLICANT: CHIRON SPA
 / APPLICANT: FONTANA Maria Rita
 / APPLICANT: PIZZA Mariagrazia
 / APPLICANT: MASIGNANI Vega
 / APPLICANT: MONACI Elisabetta
 / TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 / FILE REFERENCE:
 / CURRENT APPLICATION NUMBER: US/10/467,657
 / CURRENT FILING DATE: 2003-08-11
 / PRIOR APPLICATION NUMBER: GB-0103424.8
 / PRIOR FILING DATE: 2001-02-12
 / NUMBER OF SEQ ID NOS: 9218
 / SOFTWARE: SeqMin99, version 1.04
 / SEQ ID NO 1916
 / LENGTH: 723
 / TYPE: PRT
 / ORGANISM: Neisseria gonorrhoeae
 / US-10-467-657-1916

Query Match 51.5%; Score 34; DB 6; Length 723;
 Best Local Similarity 53.3%; Pred. No. 55;
 Matches 8; Conservative 0; Mismatches 1; Indels 6; Gaps 1;

QY 1 GPMELV-----GYF 9
 DB 260 GPMELVKSAPGYF 274

RESULT 6
 / US-10-841-129-2
 / Sequence 2, Application US/10841129
 / Publication No. US20050250113A1
 / GENERAL INFORMATION:
 / APPLICANT: Zuker, Charles S.
 / APPLICANT: Erlenbach, Isolda
 / APPLICANT: Hoon, Mark A.
 / APPLICANT: Ryba, Nicholas J. P.
 / APPLICANT: Zhang, Yifeng
 / APPLICANT: The Regents of the University of California
 / APPLICANT: The Government of the United States of America
 / APPLICANT: as represented by The Secretary of the
 / Department of Health and Human Services
 / TITLE OF INVENTION: A Mammalian Magnesium/Manganese Sensing G Protein
 / FILE REFERENCE: 023078-145400US
 / CURRENT APPLICATION NUMBER: US/10/841,129
 / CURRENT FILING DATE: 2004-05-07
 / NUMBER OF SEQ ID NOS: 7
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO 2
 / LENGTH: 926
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 / FEATURE:
 / OTHER INFORMATION: human magnesium/manganese sensing G protein
 / OTHER INFORMATION: coupled receptor (GPCR) R5.24, Mg receptor, Mn

OTHER INFORMATION: receptor
US-10-841-129-2

Query Match 51.5%; Score 34; DB 6; Length 926;
Best Local Similarity 83.3%; Pred. No. 70;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PWELVG 7
||||:|
DB 443 PWELVG 448

RESULT 7
US-11-037-829A-4
Sequence 4, Application US/11037829A
Publication No. US2005025551A1
GENERAL INFORMATION:
APPLICANT: Targacept, Inc
APPLICANT: Catholic Healthcare West
APPLICANT: Bencherif, Merouane
APPLICANT: Lukas, Ronald J.
TITLE OF INVENTION: Methods and Compositions Relating to Chimeric
TITLE OF INVENTION: Nicotinic Receptor Subunits
FILE REFERENCE: T103 1520.PCT
CURRENT APPLICATION NUMBER: US/11/037,829A
PRIOR FILING DATE: 2005-01-18
PRIOR APPLICATION NUMBER: US 60/397,380
PRIOR FILING DATE: 2002-07-19
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 478
TYPE: PRT
ORGANISM: Homo sapien
US-11-037-829A-4

Query Match 50.8%; Score 33.5; DB 7; Length 478;
Best Local Similarity 58.3%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY 1 GPWELVG---YF 9
||||:|
DB 207 GPWELVGVLPLYF 218

RESULT 8
US-11-082-389-302
Sequence 302, Application US/11082389
Publication No. US2005024935A1
GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Kroeger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
FILE REFERENCE: BGI-131CPCN
CURRENT APPLICATION NUMBER: US/11/082,389
CURRENT FILING DATE: 2005-03-16
PRIOR APPLICATION NUMBER: US 09/603024
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 60/143262
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: US 60/151281
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19930487.4
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19930489.0
PRIOR FILING DATE: 1999-07-01

PRIOR APPLICATION NUMBER: DE 19931549.3
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931550.7
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932134.5
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19941379.7
PRIOR FILING DATE: 1999-08-31
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 446
SEQ ID NO 302
LENGTH: 198
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
FEATURE:
NAME/KEY: VARIANT
LOCATION: 4
OTHER INFORMATION: Xaa = Phe, Ser, Tyr, or Cys
US-11-082-389-302

Query Match 50.0%; Score 33; DB 7; Length 198;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 WELVGY 8
||||:
DB 99 WELVGY 104

RESULT 9
US-11-082-389-304
Sequence 304, Application US/11082389
Publication No. US2005024935A1
GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Kroeger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Haberer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
FILE REFERENCE: BGI-131CPCN
CURRENT APPLICATION NUMBER: US/11/082,389
CURRENT FILING DATE: 2005-03-16
PRIOR APPLICATION NUMBER: US 09/603024
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 60/143262
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: US 60/151281
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19930487.4
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19930489.0
PRIOR FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: DE 19931549.3
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931550.7
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932134.5
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19941379.7
PRIOR FILING DATE: 1999-08-31
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 446
SEQ ID NO 304
LENGTH: 281
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-11-082-389-304

Query Match 50.0%; Score 33; DB 7; Length 281;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 MELVGY 8
|:|:|
DB 153 MQLIGY 158

RESULT 10

US-11-055-822-76
; Sequence 76, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Krogger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 76
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-76

Query Match 50.0%; Score 33; DB 7; Length 431;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPMEL 5
|:|:|
DB 284 GPMEL 288

RESULT 11

US-10-131-826A-60
; Sequence 60, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 60
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-60

Query Match 50.0%; Score 33; DB 6; Length 724;
Best Local Similarity 50.0%; Pred. No. 82;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 MELVGYFD 10
|:|:|
DB 83 WDMGYFD 90

RESULT 12

US-11-055-822-72
; Sequence 72, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Krogger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121CPN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02

```

; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 72
; LENGTH: 1510
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-72
```

Query Match 50.0%; Score 33; DB 7; Length 1510;

Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPMEL 5

DB 1063 GPMEL 1067

```

RESULT 13
US-11-113-424-52
; Sequence 52, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 2725
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-424-52
```

Query Match 50.0%; Score 33; DB 7; Length 2725;

Best Local Similarity 60.0%; Pred. No. 2.9e+02; Mismatches 4; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPMELVGYFD 10

DB 503 GPMWLAIFYND 512

```

RESULT 14
US-10-467-657-4150
; Sequence 4150, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4150
; LENGTH: 456
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4150
```

Query Match 48.5%; Score 32; DB 6; Length 456;

Best Local Similarity 57.1%; Pred. No. 78; Mismatches 2; Indels 0; Gaps 0;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PWEIVGY 8

DB 154 PWEIVGY 160

```

RESULT 15
US-11-147-047-33
; Sequence 33, Application US/11147047
; Publication No. US2005026068A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoying
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: US/11/147,047
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221,097
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-147-047-33
```

Query Match 48.5%; Score 32; DB 7; Length 533;

Best Local Similarity 83.3%; Pred. No. 90; Mismatches 1; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	2	PWELVG	7
Db	178	PWEAVG	183

Search completed: December 4, 2005, 04:37:49
Job time : 4.20833 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:09:54 / Search time 130.312 Seconds
(without alignments)
50.576 Million cell updates/sec

Title: US-10-632-706-197

Perfect score: 89
Sequence: 1 EPPDMLMGDRGALDV 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003s.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	89	100.0	15	8	ADR38727	Ad38727 Mouse hea
2	89	100.0	15	8	ADR38728	Ad38728 Mouse hea
3	89	100.0	15	8	ADR38792	Ad38792 Mouse hea
4	89	100.0	15	8	ADR38795	Ad38795 Mouse hea
5	89	100.0	15	8	ADR38798	Ad38798 Mouse hea
6	89	100.0	15	8	ADR38729	Ad38729 Mouse hea
7	75	84.3	15	8	ADR38801	Ad38801 Mouse hea
8	51	57.3	33	4	ABG20331	Abg20331 Novel hum
9	48	53.9	201	8	ADJ98189	Adj98189 Prochlo
10	48	53.9	229	7	ABO66015	Ab066015 Klebsiell
11	48	53.9	775	3	AB13560	Ab13560 Streptomy
12	47	52.8	59	2	AAV48365	Hay48365 Human pro
13	47	52.8	455	4	ABG22524	Abg22524 Novel hum
14	47	52.8	904	8	ADS23387	Ad23387 Bacterial
15	46	51.7	186	4	AAW24399	Aaw24399 Human EST
16	45	50.6	54	5	ABP03542	Abp03542 Human ORF
17	45	50.6	372	8	ABU04008	Abu04008 Protein e
18	45	50.6	450	8	ADN47961	Adn47961 Thermococ
19	45	50.6	614	7	ADF06781	Adf06781 Bacterial
20	44	49.4	70	3	AAI5847	Aai5847 Arabidops
21	44	49.4	137	6	ADA21119	Ada21119 Human sec
22	44	49.4	342	3	AAB51737	Aab51737 Human sec
23	44	49.4	409	4	AAB96393	Aab96393 Putative
24	44	49.4	472	7	ADC68881	Adc68881 Human GPC

25	44	49.4	687	8	ADS42446	Ad42446 Bacterial
26	43	48.3	100	8	ADO65091	Ad65091 Novel hum
27	43	48.3	345	2	AAV38595	Aay38595 Neisseria
28	43	48.3	345	2	ABE49036	Aeb49036 N. gonorr
29	43	48.3	383	3	AAV38596	Aay38596 Neisseria
30	43	48.3	383	6	ABP79536	Abp79536 N. gonorr
31	43	48.3	383	9	ABE49038	Aeb49038 N. gonorr
32	43	48.3	546	2	AAW26164	Aaw26164 KF-1 prot
33	43	48.3	582	4	AAU30396	Aau30396 Novel hum
34	43	48.3	616	8	ADS20416	Ad20416 Crab-eat1
35	43	48.3	683	2	AAW26163	Aaw26163 Mouse KF-
36	43	48.3	683	9	AD204210	Ad204210 Novel apo
37	43	48.3	685	2	AAW26165	Aaw26165 Human KF-
38	43	48.3	685	9	ADX07646	Adx07646 Cyclin-de
39	43	48.3	685	9	AD204207	Ad204207 Novel apo
40	43	48.3	732	9	ABW94428	Abw94428 M. xanthu
41	43	48.3	2519	7	ABW8218	Abw8218 Rice abio
42	42.5	47.8	315	4	ABW09181	Abw09181 Pseudomon
43	42.5	47.8	315	6	ABU15664	Abu15664 Protein e
44	42.5	47.8	320	7	ABO69555	Ab069555 Pseudomon
45	42	47.2	53	4	AAU65794	Aau65794 Protoninb

ALIGNMENTS

RESULT 1
ID ADR38727 standard; peptide; 15 AA.
AC ADR38727;
DT 02-DEC-2004 (first entry)
DE Mouse heavy chain variable region CDR3 seqid 129.
KW antibacterial; antibody; botulinum neurotoxin type A; BONT/A;
KW BONT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse;
KW heavy chain variable region; complementarity determining region; CDR3.
OS Mus sp.
PN US2004175365-A1.
XX
PD 09-SEP-2004.
XX
PF 01-AUG-2003; 2003US-00632706.
XX
PR 31-AUG-1998; 98US-00144886.
PR 01-AUG-2002; 2002US-0400721P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Marks JD, Amersdorfer P;
XX
DR WPI; 2004-652009/63.
XX
PT New isolated antibody that neutralizes botulinum neurotoxin type A,
PT useful for diagnosing botulism or for treating pathologies associated
PT with botulinum neurotoxin poisoning.
XX
PS Example 3; SEQ ID NO 129; 110P; English.
XX
CC The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralizes botulinum neurotoxin type A
CC (BONT/A). An isolated antibody (I) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC S25, C29, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(V), 3-1,
CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum
CC neurotoxin type A (BONT/A). Also described are: a polypeptide (II)
CC comprising BONT/A neutralising epitope having an epitope that is

CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain variable region complementarity determining
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.

XX
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 89; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDWLWMDRGALDV 15
 |||||
 Db 1 EPDWLWMDRGALDV 15

RESULT 2
 ADR38728
 ID ADR38728 standard; peptide; 15 AA.

XX ADR38728;

XX 02-DEC-2004 (first entry)

XX Mouse heavy chain variable region CDR3 seqid 130.

XX antibody; anti-botulinum neurotoxin type A; BoNT/A;

XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;

XX toxin neutralisation; botulinum neurotoxin poisoning; mouse;

XX heavy chain variable region; complementarity determining region; CDR3.

XX Mus sp.

XX US2004175385-A1.

XX 09-SEP-2004.

XX 01-AUG-2003; 2003US-00632706.

XX 31-AUG-1998; 98US-00144886.

XX 01-AUG-2002; 2002US-0400721P.

XX (REGC) UNIV CALIFORNIA.

XX Marks JD, Amersdorfer P;

XX WPI; 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.

XX Example 3; SEQ ID NO 130; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A
 CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
 CC specifically bound by an antibody expressed by a clone chosen from clone
 CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,

CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
 CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
 CC comprising BoNT/A neutralising epitope having an epitope that is
 CC specifically bound by an antibody expressed by clones as mentioned in (I)
 CC ; producing (I); and a composition (III) comprising several anti-
 CC botulinum neurotoxin antibodies, where each antibody is specific for a
 CC different epitope of a botulinum neurotoxin and the combination of
 CC antibodies shows greater toxin neutralisation than the single antibodies
 CC in surplus. The following are disclosed: a pharmaceutical composition
 CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
 CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
 CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
 CC specific for a different epitope of the botulinum neurotoxin and the
 CC combination of antibodies shows greater toxin neutralisation than the
 CC single antibodies in surplus. (I) is useful for diagnosing the botulism
 CC or for treating pathologies associated with botulinum neurotoxin
 CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
 CC enables rapid detection or diagnosis of botulism. This is the amino acid
 CC sequence of mouse heavy chain variable region complementarity determining
 CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.

XX
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 89; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDWLWMDRGALDV 15
 |||||
 Db 1 EPDWLWMDRGALDV 15

RESULT 3
 ADR38792
 ID ADR38792 standard; peptide; 15 AA.

XX ADR38792;

XX 02-DEC-2004 (first entry)

XX Mouse heavy chain anti-BoNT-antibody CDR3 seqid 194.

XX antibody; anti-BoNT-antibody; botulinum neurotoxin type A; BoNT/A;

XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;

XX toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
 KW CDR3; complementarity determining region 1.

XX Mus sp.

XX US2004175385-A1.

XX 09-SEP-2004.

XX 01-AUG-2003; 2003US-00632706.

XX 31-AUG-1998; 98US-00144886.

XX 01-AUG-2002; 2002US-0400721P.

XX (REGC) UNIV CALIFORNIA.

XX Marks JD, Amersdorfer P;

XX WPI; 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,
 PT useful for diagnosing botulism or for treating pathologies associated
 PT with botulinum neurotoxin poisoning.

XX Example 4; SEQ ID NO 194; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds
 CC to an epitope specifically bound by an antibody expressed by a specific
 CC clone where (I) binds to and neutralises botulinum neurotoxin type A

(BoNT/A). An isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a clone chosen from clone CC S25, C25, C39, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1, CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum neurotoxin type A (BoNT/A). Also described are: a polypeptide (II) comprising BoNT/A neutralising epitope having an epitope that is specifically bound by an antibody expressed by clones as mentioned in (I) ; producing (I) ; and a composition (III) comprising several anti-botulinum neurotoxin antibodies, where each antibody is specific for a different epitope of a botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. The following are disclosed: a pharmaceutical composition comprising (I) ; and a kit comprising (I). (I) is useful for neutralising BoNT/A antibody and for neutralising a botulinum neurotoxin which involves contacting neurotoxin with (I) in surplus, where each of (I) is specific for a different epitope of the botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. (I) is useful for diagnosing the botulinum or for creating pathologies associated with botulinum neurotoxin poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I) enables rapid detection or diagnosis of botulinism. This is the amino acid sequence of mouse heavy chain anti-BoNT-antibody CDR3.

Seq Sequence 15 AA;

Query Match 100.0%; Score 89; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDWLMGDRGALDV 15
| | | | | | | | | | | | | | | | |
Db 1 EPDWLMGDRGALDV 15

RESULT 4
ADR38795
ID ADR38795 standard; peptide; 15 AA.

AC ADR38795;
XX
DT 02-DEC-2004 (first entry)

DE Mouse heavy chain anti-BoNT-antibody CD3 seqid 197.

XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
XX toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
XX CDR3; complementarity determining region 1.

OS Mus sp.

PN US2004175385-A1.

PD 09-SEP-2004.

PF 01-AUG-2003; 2003US-00632706.

PR 31-AUG-1998; 98US-00144886.

PR 01-AUG-2002; 2002US-0400721P.

PA (REGC) UNIV CALIFORNIA.

PI Marke JD, Amersdorfer P;

DR WPI; 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,
XX useful for diagnosing botulinism or for treating pathologies associated
XX with botulinum neurotoxin poisoning.
XX Example 4; SEQ ID NO 197; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds

to an epitope specifically bound by an antibody expressed by a specific clone where (I) binds to and neutralises botulinum neurotoxin type A (BoNT/A). An isolated antibody (I) that specifically binds to an epitope specifically bound by an antibody expressed by a clone chosen from clone CC S25, C25, C39, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1, CC 3-8, 3-10 and INGI, where (I) binds to and neutralizes botulinum neurotoxin type A (BoNT/A). Also described are: a polypeptide (II) comprising BoNT/A neutralising epitope having an epitope that is specifically bound by an antibody expressed by clones as mentioned in (I) ; producing (I) ; and a composition (III) comprising several anti-botulinum neurotoxin antibodies, where each antibody is specific for a different epitope of a botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. The following are disclosed: a pharmaceutical composition comprising (I) ; and a kit comprising (I). (I) is useful for neutralising BoNT/A antibody and for neutralising a botulinum neurotoxin which involves contacting neurotoxin with (I) in surplus, where each of (I) is specific for a different epitope of the botulinum neurotoxin and the combination of antibodies shows greater toxin neutralisation than the single antibodies in surplus. (I) is useful for diagnosing the botulinum or for creating pathologies associated with botulinum neurotoxin poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I) enables rapid detection or diagnosis of botulinism. This is the amino acid sequence of mouse heavy chain anti-BoNT-antibody CDR3.

Seq Sequence 15 AA;

Query Match 100.0%; Score 89; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDWLMGDRGALDV 15
| | | | | | | | | | | | | | | | |
Db 1 EPDWLMGDRGALDV 15

RESULT 5
ADR38798
ID ADR38798 standard; peptide; 15 AA.

AC ADR38798;

DT 02-DEC-2004 (first entry)

DE Mouse heavy chain anti-BoNT-antibody CD3 seqid 200.

XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
XX toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
XX CDR3; complementarity determining region 1.

OS Mus sp.

PN US2004175385-A1.

PD 09-SEP-2004.

PF 01-AUG-2003; 2003US-00632706.

PR 31-AUG-1998; 98US-00144886.

PR 01-AUG-2002; 2002US-0400721P.

PA (REGC) UNIV CALIFORNIA.

PI Marke JD, Amersdorfer P;

DR WPI; 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,
XX useful for diagnosing botulinism or for treating pathologies associated
XX with botulinum neurotoxin poisoning.
XX Example 4; SEQ ID NO 200; 110pp; English.

XX The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralizes botulinum neurotoxin type A
CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC S25, C39, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
CC 3-8, 3-10 and INC1, where (I) binds to and neutralizes botulinum
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
CC comprising BoNT/A neutralising epitope having an epitope that is
CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC ; producing (I); and a composition (III) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain anti-BoNT-antibody CDR3.
SQ Sequence 15 AA;

Query Match 100.0%; Score 89; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDMLMGDRGALDV 15
| | | | | | | | | | | | | | |
Db 1 EPDMLMGDRGALDV 15

RESULT 6
ADR38729
ID ADR38729 standard; peptide; 15 AA.
XX
AC ADR38729;
XX
DT 02-DEC-2004 (first entry)
XX

DE Mouse heavy chain variable region CDR3 seqid 131.

XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
XX toxin neutralisation; botulinum neurotoxin poisoning; mouse;
XX heavy chain variable region; complementarity determining region; CDR3.

OS Mus sp.

PN US2004175385-A1.

PD 09-SEP-2004.

PF 01-AUG-2003; 2003US-00632706.

PR 31-AUG-1998; 98US-00144886.

XX 01-AUG-2002; 2002US-0400721P.

PA (REGC) UNIV CALIFORNIA.

PI Marks JD, Amerdorfer P;

XX MPI; 2004-652009/63.

XX New isolated antibody that neutralizes botulinum neurotoxin type A,
PT useful for diagnosing botulism or for treating pathologies associated
PT with botulinum neurotoxin poisoning.

XX Example 3; SEQ ID NO 131; 110pp; English.

PS The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralizes botulinum neurotoxin type A
CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC S25, C39, C39, 1C6, 3D12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
CC 3-8, 3-10 and INC1, where (I) binds to and neutralizes botulinum
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
CC comprising BoNT/A neutralising epitope having an epitope that is
CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC ; producing (I); and a composition (III) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain variable region complementarity determining
CC region 3 (CDR3) from anti-botulinum neurotoxin antibodies.
SQ Sequence 15 AA;

Query Match 100.0%; Score 89; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDMLMGDRGALDV 15
| | | | | | | | | | | | | | |
Db 1 EPDMLMGDRGALDV 15

RESULT 7
ADR38801
ID ADR38801 standard; peptide; 15 AA.
XX
AC ADR38801;
XX
DT 02-DEC-2004 (first entry)
XX

DE Mouse heavy chain anti-BoNT-antibody CDR3 seqid 203.

XX antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
XX BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
XX toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
XX CDR3; complementarity determining region 1.

OS Mus sp.

PN US2004175385-A1.

PD 09-SEP-2004.

PF 01-AUG-2003; 2003US-00632706.

PR 31-AUG-1998; 98US-00144886.

XX 01-AUG-2002; 2002US-0400721P.

PA (REGC) UNIV CALIFORNIA.

PI Marks JD, Amerdorfer P;

XX MPI; 2004-652009/63.

PT New isolated antibody that neutralizes botulinum neurotoxin type A.
PT Useful for diagnosing botulism or for treating pathologies associated
PT with botulinum neurotoxin poisoning.
PS Example 4; SEQ ID NO 203; 110pp; English.
XX
CC The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralises botulinum neurotoxin type A
CC (BoNT/A). An isolated antibody (II) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC S25, C39, 106, 3d12, B4, 1F3, huc25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
CC comprising BoNT/A neutralising epitope having an epitope that is
CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC ; producing (I); and a composition (III) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain anti-BoNT-antibody CDR3.
XX
SQ Sequence 15 AA;
XX
Query Match 84.3%; Score 75; DB 8; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00023;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EPPDWILMGDRGALDV 15
DB 1 EPPDWILMGDRGALDV 15
XX
RESULT 8
ABG20331
ID ABG20331 standard; protein; 334 AA.
XX
AC ABG20331;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #20322.
XX
KW Human; chromosome mapping; gene mapping; forensic;
KW Food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
XX
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS84518.
DR

XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 50690; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 334 AA;
XX
Query Match 57.3%; Score 51; DB 4; Length 334;
Best Local Similarity 53.3%; Pred. No. 23;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 EPPDWILMGDRGALDV 15
DB 263 KPDMSWGPSSGWIDV 277
XX
RESULT 9
ADJ98189
ID ADJ98189 standard; protein; 201 AA.
XX
AC ADJ98189;
XX
DT 06-MAY-2004 (first entry)
XX
DE Prochlorococcus marinus str MIT 9313 phycol kinase protein.
XX
KW phycol kinase; tocopherol biosynthesis; plant; drought resistance;
KW enzyme.
XX
OS Prochlorococcus marinus str. MIT 9313.
XX
PN WO2004013312-A2.
XX
PD 12-FEB-2004.
XX
PF 05-AUG-2003; 2003WO-US025276.
XX
PR 05-AUG-2002; 2002US-0400689P.
XX
PR 05-AUG-2003; 2003US-00634548.
XX
PA (MONS) MONSANTO TECHNOLOGY LLC.
XX
PI Norris SR, Lincoln K, Abad MS, Eilers R, Hartuyker KK;
PI Hirschberg J, Karunanandaa B, Moshiri F, Stein JC, Valentin HB;
PI Venkatesh TV;
XX
DR WPI; 2004-157125/15.
DR

PT New phycol kinase polynucleotides, useful in mediating tocopherol
PT biosynthesis and in producing plants with increased drought resistance.
XX
PS Claim 1, SEQ ID NO 27, 18pp; English.

XX DE1981194-A1.
 XX 16-SEP-1999.
 PD 10-MAR-1998; 98DE-01011194.
 PF 10-MAR-1998; 98DE-01011194.
 XX 10-MAR-1998; 98DE-01011194.
 PR (META-) METAGEN GES GENOMFORSCHUNG MBH.
 XX
 XX Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
 PI WPI; 1999-519629/44.
 DR N-PSDB; AA233505.
 XX
 PT New nucleic acid expressed at high level in normal prostatic tissue and
 PT encoded polypeptides, used to treat cancer and screen for therapeutic
 PT agents.
 XX
 XX Claim 22; 148; 194p; German.
 PS
 CC This invention describes novel nucleic acid sequences (A) that are
 CC expressed at high level in normal prostatic tissue. Polypeptides (I)
 CC encoded by (A) are used: (a) for identifying agents for treatment of
 CC prostatic cancer and (b) for therapy of prostate cancer, optionally where
 CC expressed by gene therapy methods. (A) is also used to isolate full-
 CC length genes (for gene therapy) and for recombinant production of (I),
 CC which can be used to raise specific antibodies. (A) are identified by
 CC assembly of ESTs (expressed sequence tags) before these are analyzed for
 CC expression pattern (tissue specificity). This approach eliminates many of
 CC the false results, as regards tissue specificity, associated with known
 CC methods that use single (usually short) ESTs. AA148304-Y48456 represent
 CC peptides encoded by the expressed sequence tags described in the method
 CC of the invention
 CC
 SQ Sequence 59 AA;
 XX
 XX Query Match 52.8%; Score 47; DB 2; Length 59;
 XX Best Local Similarity 87.5%; Pred. No. 15;
 XX Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 WLMGDRG 11
 DB 44 WLMGSRG 51
 XX
 XX RESULT 13
 XX ABG22524
 ID ABG22524 standard; protein; 455 AA.
 XX
 XX ABG22524;
 AC
 XX
 DT 18-FEB-2002 (first entry)
 XX
 XX Novel human diagnostic protein #22515.
 DE
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX

PI Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 DR N-PSDB; AAS86711.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 XX Claim 20; SEQ ID NO 52883; 103p; English.
 PS
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 455 AA;
 XX
 XX Query Match 52.8%; Score 47; DB 4; Length 455;
 XX Best Local Similarity 53.8%; Pred. No. 1.3e+02;
 XX Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EPDWLMLGDRGAL 13
 DB 93 EQNWLMLCERGVN 105
 XX
 XX RESULT 14
 XX ADS23387
 ID ADS23387 standard; protein; 904 AA.
 XX
 XX ADS23387;
 AC
 XX
 DT 02-DEC-2004 (first entry)
 XX
 XX Bacterial polypeptide #12420.
 DE
 XX Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmotic;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactanmanan;
 KW bacterial polypeptide.
 XX
 OS Bacteria.
 XX
 PN US2003233675-A1.
 XX
 PD 18-DEC-2003.
 XX
 PF 20-FEB-2003; 2003US-00369493.
 XX
 PR 21-FEB-2002; 2002US-0360039P.
 XX

PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX
 PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX
 DR WPI, 2004-061375/06.
 XX
 PT New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 PS Claim 1, SEQ ID NO 12420; 122pp; English.
 XX
 CC The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Notes: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 CC
 SQ Sequence 904 AA;
 QY
 DB 460 WLMGDKTSL 469
 QY 4 WLMGDKTSL 13
 DB 460 WLMGDKTSL 469
 RESULT 15
 AAM24399
 ID AAM24399 standard; protein; 186 AA.
 AC
 XX AAM24399;
 XX
 DT 12-OCT-2001 (first entry)
 XX
 DE Human EST encoded protein SEQ ID NO: 1924.
 XX
 XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 XX tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 XX diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
 XX gene therapy; nutrition.
 OS Homo sapiens.
 XX
 XX MO200154477-A2.
 PN
 XX 02-AUG-2001.
 PD
 XX

PF 25-JAN-2001; 2001WO-US002687.
 XX
 XX 25-JAN-2000; 2000US-00491404.
 PR 17-JUL-2000; 2000US-00617746.
 PR 03-AUG-2000; 2000US-00631451.
 PR 15-SEP-2000; 2000US-0063870.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YF, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Aundl V;
 PI Cao Y, Dermanac RA, Zhang J, Werhman T;
 XX
 DR WPI: 2001-476164/51.
 DR N-PSDB; AAH99058.
 XX
 PT Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use.
 XX
 PS Claim 20; Page 1235; 1275pp; English.
 XX
 CC The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a
 CC protein of the invention
 CC
 SQ Sequence 186 AA;
 QY
 DB 168 PGMWIMGKXNKGILN 182
 QY 2 PGMWIMG--DRGALD 14
 DB 168 PGMWIMGKXNKGILN 182
 Search completed: December 4, 2005, 04:44:59
 Job time : 132.312 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 4, 2005, 04:31:45 ; Search time 21.25 Seconds
(without alignments)
67,918 Million cell updates/sec

Title: US-10-632-706-197

Perfect score: 89
Sequence: 1 EPDMLMGDRGALDV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	51.7	373	2 D71142	hypothetical prote
2	45.5	51.1	298	2 AB3234	transcriptional re
3	45	50.6	203	2 G70595	probable entd prot
4	45	50.6	601	2 AG0066	probable AMP-bindi
5	44.5	50.0	1076	2 T30842	serine-repeat anti
6	44	49.4	237	2 G82768	virulence protein
7	44	49.4	409	2 B75010	hypothetical prote
8	44	49.4	491	2 T10930	3C3.21 protein - S
9	44	49.4	601	2 E95296	probable ABC-type
10	43	48.3	321	2 S77614	phosphoribosylform
11	43	48.3	462	2 T50422	homolog to yeast o
12	43	48.3	683	2 JC5393	zinc finger protei
13	43	48.3	685	2 JC5392	zinc finger protei
14	43	48.3	698	2 A82593	hypothetical prote
15	42.5	47.8	315	2 H83276	probable lipase PA
16	42	47.2	71	2 G98356	hypothetical prote
17	42	47.2	139	2 AG2925	hypothetical prote
18	42	47.2	397	2 E53240	allergen Amb a II
19	42	47.2	408	1 A69819	probable phosphoe
20	42	47.2	482	1 A10554	thiamin biosynthes
21	42	47.2	482	2 E90688	probable oxidoredu
22	42	47.2	482	2 T46944	thiamin biosynthes
23	42	47.2	482	2 A85539	probable oxidoredu
24	42	47.2	482	2 G64771	yaJk protein - Bsc
25	42	47.2	486	2 T51431	glucosyltransferas
26	42	47.2	486	2 H87311	hypothetical prote
27	42	47.2	492	2 T38156	citrate lyase - fl
28	42	47.2	566	2 H84037	long-chain fatty-a
29	42	47.2	604	2 T49577	hypothetical prote

30	42	47.2	608	2 T34994	probable long-chain
31	42	47.2	804	2 AG0565	probable membrane
32	42	47.2	804	2 G64780	probable membrane
33	42	47.2	804	2 A85549	probable oxidoredu
34	42	47.2	804	2 G90698	probable oxidoredu
35	42	47.2	993	2 B97219	conserved membrane
36	41	46.1	36	2 B84416	hypothetical prote
37	41	46.1	248	2 T36093	probable DNA methy
38	41	46.1	262	2 F75093	hypothetical prote
39	41	46.1	288	2 AG0888	probable Arac-fam1
40	41	46.1	359	2 C70735	probable idsa prot
41	41	46.1	403	2 T10847	y4M protein - Rhl
42	41	46.1	408	2 AG0305	probable L-iditol
43	41	46.1	438	2 T37786	probable RNA-bindi
44	41	46.1	442	2 D84600	probable xylose
45	41	46.1	459	2 T27657	hypothetical prote

ALIGNMENTS

RESULT 1
D71142
hypothetical protein PH0351 - *Pyrococcus horikoshii*
C/Species: *Pyrococcus horikoshii*
C/Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 09-Jul-2004
R/Accession: D71142
R/Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kuchida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A/Reference number: A71000; MUID:98344137; PMID:9679194
A/Accession: D71142
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-373 <KAW>
A/Cross-references: UNIPROT:O58089; UNIPARC:UPI0000062DB7; GB:AP000002; NID:93236129; PI
A/Experimental source: strain OT3
A/Note: This accession replaces an interim accession for a sequence replaced by GenBank
C/Genetics:
A/Gene: PH0351

Query Match 51.7% Score 46; DB 2; Length 373;
Best Local Similarity 43.5%; Pred. No. 19;
Matches 10; Conservative 1; Mismatches 2; Indels 10; Gaps 1;

QY 2 PDMLM-----GDRGALD 14
Db 318 PGMILMGLILMGRIGNPGALD 340

RESULT 2
AB3234
transcriptional regulator, *lyrS* family *gcva* [imported] - *Agrobacterium tumefaciens* (stra
C/Species: *Agrobacterium tumefaciens*
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
R/Accession: AB3234
R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erge, G.; Gillitt, W.; Grant, C.; Guenther, D.; Kuyavain, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A/Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A/Reference number: AB2577; MUID:21608550; PMID:11743193
A/Accession: AB3234
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-298 <KUR>
A/Cross-references: UNIPROT:O8U680; UNIPARC:UPI0000002764; GB:AE008690; PIDN:AA146291.1;
A/Experimental source: strain C58 (Dupont)
C/Genetics:
A/Gene: *gcva*

RESULT 7

hypothetical protein PAB1063 - *Pyrococcus abyssi* (strain Orya)
 B75010
 C:Species: *Pyrococcus abyssi*
 C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
 C:Accession: B75010
 R:anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A:Description: *Pyrococcus abyssi* genome sequence: insights into archaeal chromosome stru
 A:Reference number: A75001
 A:Accession: B75010
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-409 <KAM>
 A:Cross-references: UNIPROT:Q9Y92; UNIPARC:UPI0000034560; GB:AJ248288; GB:AL056836; NID
 C:Experimental source: strain Orya
 C:Genetics:
 A:Gene: PAB1063

Query Match

49.4%; Score 44; DB 2; Length 409;
 Best Local Similarity 39.1%; Pred. No. 41;
 Matches 9; Conservative 2; Mismatches 2; Indels 10; Gaps 1;

QY 2 PDWLM-----GDRGALD 14
 |||||
 DB 354 PGWILGILILMGVRGNCALD 376

RESULT 8

3C3.21 protein - *Streptomyces coelicolor*
 T10930
 C:Species: *Streptomyces coelicolor*
 C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C:Accession: T10930
 R:Parkhill, J.; Barrett, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, August 1998
 A:Reference number: Z17215
 A:Accession: T10930
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-491 <PAR>
 A:Cross-references: UNIPROT:O86654; UNIPARC:UPI00000DAD67; EMBL:AL031231; NID:e1315070;
 A:Experimental source: strain A3 (2)
 C:Genetics:
 A:Gene: 3C3.21

Query Match

49.4%; Score 44; DB 2; Length 491;
 Best Local Similarity 61.5%; Pred. No. 49;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 DMLMGDRGALDV 15
 :|||
 DB 413 EFWLHGDGRALDL 425

RESULT 9

probable ABC-type iron transport system protein Sma0525 [imported] - *Sinorhizobium meliloti*
 E95296
 C:Species: *Sinorhizobium meliloti*
 C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C:Accession: E95296
 R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe
 ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A:Title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti*
 A:Reference number: A95262; MUID:2136509; PMID:11481432
 A:Accession: E95296
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-601 <KUR>
 A:Cross-references: UNIPROT:Q930C1; UNIPARC:UPI00000C803E; GB:AE006469; PIDN:AAK64935.1;
 A:Experimental source: strain 1021, megaplasmid pSymA

R.Gallbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 Pala, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 hebbaut, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A:Title: The complete genome of the legume symbiont *Sinorhizobium meliloti*.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: Sma0525
 A:Genome: plasmid

Query Match

49.4%; Score 44; DB 2; Length 601;
 Best Local Similarity 85.7%; Pred. No. 59;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PDWLMG 8
 |||||
 DB 169 PDWLMWG 175

RESULT 10

S77614
 phosphoribosylformylglycinamide synthase (EC 6.3.5.3) component II - *Synechococcus* sp
 N:Alternate names: FGA synthetase
 C:Species: *Synechococcus* sp.
 A:Variety: PCC 7942
 C>Date: 29-Jul-1997 #sequence_revision 24-Oct-1998 #text_change 31-Dec-2004
 C:Accession: S77614; S77613
 R:Lin, Y.; Tsinoremas, N.F.
 submitted to the EMBL Data Library, August 1995
 A:Description: Unusual gene arrangement for the putative chromosome replication origin a
 A:Reference number: S77614
 A:Accession: S77614

A:Molecule type: DNA
 A:Residues: 1-112 <LIV>
 A:Cross-references: UNIPROT:O55037; UNIPARC:UPI0000176276; EMBL:U33322; NID:g974613; PID
 A:Experimental source: PCC 7942
 R:Lin, Y.; Tsinoremas, N.F.; Golden, S.S.; Kondo, T.; Johnson, C.H.
 Mol. Microbiol. 20, 1071-1081, 1996
 A:Title: Circadian expression of genes involved in the purine biosynthetic pathway of *cy*

A:Reference number: S77612; MUID:96405630; PMID:8809759
 A:Accession: S77613
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 113-321 <LIV>

A:Cross-references: UNIPARC:UPI0000BEA44; EMBL:U33211
 A:Experimental source: PCC 7942
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
 C:Genetics:
 A:Gene: purL

C:Function:
 A:Description: catalyzes the condensation of 5'-phosphoribosylformylglycinamide with ATP
 A:Pathway: purine nucleotide biosynthesis
 A:Note: fourth step in pathway
 C:Keywords: ligase; purine nucleotide biosynthesis

Query Match

48.3%; Score 43; DB 2; Length 321;
 Best Local Similarity 63.6%; Pred. No. 46;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PDWLMGDRGA 12
 |||||
 DB 240 PDWLMFAEGGA 250

RESULT 11

T50422
 homolog to yeast orf yor166c. [imported] - fission yeast (*Schizosaccharomyces pombe*)
 C:Species: *Schizosaccharomyces pombe*
 C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
 C:Accession: T50422

R.Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 Submitted to the EMBL Data Library, February 2000
 A:Reference number: Z25039
 A:Accession: T50422
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-462 <SRS>
 A:Cross-references: UNIPROT:O9P7J1; UNIPARC:UPI000006A1B; EMBL:AL157991; PIDN:CAE76224.
 A:Experimental source: strain 972h(-); coemid c24B10
 C:Genetics:
 A:Gene: SPDB:SPCC24B10.15
 A:Map position: 3

Query Match 48.3%; Score 43; DB 2; Length 462;
 Best Local Similarity 55.6%; Pred. No. 65;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 DMLMGDRG 11
 |||||
 Db 394 EEWLWABRG 402

RESULT 12
 JCS393
 zinc finger protein KF-1 precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 04-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
 C:Accession: JCS393
 R.Yaaojima, K.; Tsujimura, A.; Mizuno, T.; Shigeyoshi, Y.; Inazawa, J.; Kikuno, R.; Kuma
 Biochem. Biophys. Res. Commun. 231, 481-487, 1997
 A:Title: Cloning of human and mouse cDNAs encoding novel zinc finger proteins expressed
 A:Reference number: JCS392; MUID:97223484; PMID:9070305
 A:Accession: JCS393
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-683 <YAS>
 A:Cross-references: UNIPROT:O08883; UNIPARC:UPI000008061; DBJ:D76445; NID:g2058262; PI
 A:Experimental source: brain
 C:Comment: This protein is involved in membranous protein-sorting apparatus similarly to
 C:Genetics:
 A:Gene: Kf-1
 C:Superfamily: zinc finger protein KF-1 precursor; RING finger homology
 C:Keywords: glycoprotein; phosphoprotein; zinc
 F.1-19/Domain: signal sequence #status predicted <SIG>
 F.326-344/Domain: transmembrane #status predicted <TM2>
 F.352-380/Domain: transmembrane #status predicted <TM2>
 F.615-666/Domain: RING finger homology <RING>
 F.100,155,228,273,301,398,536/Binding site: carbohydrate (Asn) (covalent) #status predic
 F.664/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 48.3%; Score 43; DB 2; Length 683;
 Best Local Similarity 85.7%; Pred. No. 95;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EPDWLW 7
 |||||
 Db 603 EPDWLW 609

RESULT 13
 JCS392
 zinc finger protein KF-1 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 04-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
 C:Accession: JCS392
 R.Yaaojima, K.; Tsujimura, A.; Mizuno, T.; Shigeyoshi, Y.; Inazawa, J.; Kikuno, R.; Kuma
 Biochem. Biophys. Res. Commun. 231, 481-487, 1997
 A:Title: Cloning of human and mouse cDNAs encoding novel zinc finger proteins expressed
 A:Reference number: JCS392; MUID:97223484; PMID:9070305
 C:Accession: JCS392
 A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA
 A:Residues: 1-685 <YAS>
 A:Cross-references: UNIPROT:O00237; UNIPARC:UPI00000732A; DBJ:D76444; NID:g1945614; PI
 A:Experimental source: brain
 C:Comment: This protein is involved in membranous protein-sorting apparatus similarly to
 C:Genetics:
 A:Gene: Kf-1
 C:Superfamily: zinc finger protein KF-1 precursor; RING finger homology
 C:Keywords: zinc
 F.1-19/Domain: signal sequence #status predicted <SIG>
 F.326-344/Domain: transmembrane #status predicted <TM2>
 F.352-380/Domain: transmembrane #status predicted <TM2>
 F.617-668/Domain: RING finger homology <RING>

Query Match 48.3%; Score 43; DB 2; Length 685;
 Best Local Similarity 85.7%; Pred. No. 95;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EPDWLW 7
 |||||
 Db 605 EPDWLW 611

RESULT 14
 A82593
 hypothetical protein XF2169 [imported] - Xylella fastidiosa (strain 945C)
 C:Species: Xylella fastidiosa
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C:Accession: A82593
 R.anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: A82515; MUID:20365717; PMID:10910347
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: A82593
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-698 <SIM>
 A:Cross-references: UNIPROT:O9PBH5; UNIPARC:UPI00000C2968; GB:AB004030; GB:AB003849; NID
 A:Experimental source: strain 945C
 R.Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
 B.Rios, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
 as-Neto, E.; Docena, C.; El-Dorcy, H.; Facinani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Froma
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitejima, J.P.; Kiesecker, J.E.; Kuremaa, E.E.; Laigr
 Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martins, C.L.; Marques, M.V.; Martins, E
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savasak
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tsunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:
 A:Gene: XF2169

Query Match 48.3%; Score 43; DB 2; Length 698;
 Best Local Similarity 63.6%; Pred. No. 97;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 DMLMGDRGAL 13
 |||||
 Db 554 DMLMGDRGSL 564

RESULT 15
 H83276
 probable lipase PA2949 [imported] - Pseudomonas aeruginosa (strain PAO1)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 12-Jul-2004
 C:Accession: H83276
 R.Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Lardig, K.; Lim,
.: Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: H83276
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-315 <STO>
A:Cross-references: UNIPROT:O9KJG6; UNIPARC:UPI00000C4EC6; GB:AE004721; GB:AE004091; NID
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2949
C:Superfamily: tropinesterase

Query Match 47.8%; Score 42.5; DB 2; Length 315;
Best Local Similarity 66.7%; Pred. No. 54;
Matches 10; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
Qy 2 PDLWGDRC-ALDV 15
| | | | | | | | | |
Db 249 PTLWGDRCRDVLDV 263

Search completed: December 4, 2005, 04:53:46
Job time : 33.25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:36 ; Search time 136.875 Seconds
(without alignments)
77.318 Million cell updates/sec

Title: US-10-632-706-197

Perfect score: 89
Sequence: 1 EPDMLMGDRGALDV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	56.2	441	2	Q5LQ90_SILPO
2	49	55.1	208	2	Q5YQ86_NOCFA
3	49	55.1	405	2	Q5N4J9_SYNP6
4	49	55.1	779	2	Q6H084_FREDD
5	48	53.9	217	2	Q7V3U3_PROWM
6	48	53.9	252	2	Q8EJF9_SHEON
7	48	53.9	426	2	Q5SS50_CRYNE
8	48	53.9	448	2	Q9S4Z3_SALEN
9	48	53.9	775	2	Q9S8A1_CANAL
10	48	53.9	784	2	Q8GM13_STRGL
11	48	53.9	793	2	Q59870_CANAL
12	48	53.9	804	2	Q8ZB90_SALTY
13	47.5	53.4	527	2	Q6ZDZ2_ORYSA
14	47	52.8	61	2	Q6UHZ8_HUMAN
15	47	52.8	364	2	Q7UG34_RHOMA
16	47	52.8	369	2	Q5KXN7_CRYNE
17	47	52.8	375	2	Q55ZB2_CRYNE
18	47	52.8	471	2	Q4TPV5_SSPHN
19	47	52.8	1517	2	Q5AIP9_EBENT
20	47	52.8	1547	2	Q9C1A0_ASPPU
21	47	52.8	1547	2	Q4WDD4_ASPPU
22	46	51.7	214	2	Q4JX96_CORJK
23	46	51.7	350	1	COBT_PBSRM
24	46	51.7	356	2	Q6C1B2_YARLI
25	46	51.7	373	2	Q58089_PYRHO
26	46	51.7	396	2	Q70GK6_CHLRS
27	46	51.1	1562	2	Q9Y840_MYCGR
28	45.5	51.1	266	2	Q7D2M8_AGRFS
29	45.5	51.1	298	2	Q8U680_AGRFS
30	45	50.6	91	2	Q85AE3_GCARD
31	45	50.6	141	2	Q9NU66_HUMAN

32	45	50.6	203	2	Q6MWZ7_MYCTU	Q6mwz7 mycobacteri
33	45	50.6	228	2	Q7TWZ8_MYCBO	Q7twz8 mycobacteri
34	45	50.6	203	2	Q7DSX2_MYCTU	Q7dsx2 mycobacteri
35	45	50.6	246	2	Q7U9T4_SYNPX	Q7u9t4 synchococc
36	45	50.6	370	2	Q8BJL2_SYNPX	Q8bjl2 synchococc
37	45	50.6	381	2	Q5P2Z9_AZOSE	Q5p2z9 azococcus sp
38	45	50.6	450	2	Q5JDB4_PYROK	Q5jdb4 pyrococcus
39	45	50.6	505	2	Q5LR06_SILPO	Q5lrg6 silicibacte
40	45	50.6	601	2	Q6EEL9_YERPS	Q6eel9 yerisinta ps
41	45	50.6	601	2	Q8Z1G5_YERPE	Q8z1g5 yerisinta pe
42	45	50.6	781	2	Q4HYZ0_GIBZB	Q4hyz0 gibbeteila
43	45	50.6	892	2	Q4KIVA_PSEFP	Q4kiva pseudomonas
44	45	50.6	907	2	Q4ZNE9_PSEPS	Q4zne9 pseudomonas
45	45	50.6	1326	2	Q6ATH6_ORYSA	Q6ath6 oryza sativ

ALIGNMENTS

```
RESULT 1
Q5LQ90_SILPO PRELIMINARY; PRT; 441 AA.
AC Q5LQ90;
DT 01-FEB-2005 (TREMBlrel. 29, Created)
DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
DE TRAP dicarboxylate transporter, DctW subunit.
GN OrderedLocustNames=SP02605;
OS Silicibacter pomeroyi.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Silicibacter.
OX NCBI_TaxID=89184;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=DS-3 / ATCC 700808 / DSM 15171;
RX PubMed=15602564; DOI=10.1038/nature03170;
RA Moran M.A., Buchan A., Gonzalez J.M., Heidelberg J.F., Whitman W.B.,
RA Kiene R.P., Henriksen J.R., King G.W., Belas R., Fugua C.,
RA Brinkac L.M., Lewis M., Jothi S., Weaver B., Pal G., Bisen J.A.,
RA Rahe B., Sheldon W.M., Ye W., Miller T.R., Carlton J., Raeko D.A.,
RA Paulsen I.T., Ren Q., Daugherty S.C., Deboy R.T., Dodson R.J.,
RA Durlin A.S., Madupu R., Nelson W.C., Sullivan S.A., Rosovitz M.J.,
RA Haft D.H., Selengut J., Ward N.;
RT "Genome sequence of Silicibacter pomeroyi reveals adaptations to the
RT marine environment."
RL Nature 432:910-913(2004).
DR EMBL: CP000031; AAV95851.1; -; Genomic_DNA.
DR InterPro: IPR010656; DctW.
DR InterPro: IPR000252; DctW.
DR Pfam: PF06808; DctW; 1.
KW Pfam; PF00597; DctW; 1.
KW Complete proteome.
SQ SEQUENCE 441 AA; 48056 MW; 8E59B0X46Z757858 CRC64;

Query Match Score 50; DB 2; Length 441;
Best Local Similarity 72.7%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Nocardia; Nocardia.
OX NCBI_TaxID=37329;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IFM 10152;
RX PubMed=15466710; DOI=10.1073/pnas.0406410101;
RA Ishikawa J., Yamashita A., Mikami Y., Hoshino Y., Kurita H., Hotta K.,
RA Shiba T., Hatfort M.;
RT "The complete genomic sequence of Nocardia farcinica IFM 10152."
RL Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).
DR EMBL; AP006618; BAD59655.1; -; Genomic_DNA.
KM Complete proteome; Hypothetical protein.
SQ SEQUENCE 208 AA; 22565 MW; EBE3243D9E52094E CRC64;

Query Match 55.1%; Score 49; DB 2; Length 208;
Best Local Similarity 46.7%; Pred. No. 16;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPDWLMGDRGALDV 15
Db 111 DEDWYMLNRDRIDV 125

RESULT 3
OSN4J9 SYN6 PRELIMINARY; PRT; 405 AA.
ID OSN4J9 SYN6 PRELIMINARY;
AC OSN4J9;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Sun protein.
GN Name=sun; OrderedLocustNames=syc0580.d;
OC Synecococcus sp. (strain PCC 6301) (Anacyetis nidulans).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=269084;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PCC6301;
RA Sugita M.;
RT "Complete genome structure of the unicellular cyanobacterium Anacyetis
RT nidulans 6301 (Synecococcus sp. PCC6301).";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP008231; BAD78770.1; -; Genomic_DNA.
DR GO; GO:0008649; F:RNA methyltransferase activity; IEA.
DR GO; GO:0006364; P:RNA processing; IEA.
DR InterPro; IPR004573; Fmu_mtrase.
DR InterPro; IPR001678; Fmu_NOL1/NOP2p.
DR InterPro; IPR006027; NubB_Ramb_TIM4.
DR InterPro; IPR006174; RmbB_mtfase.
DR InterPro; IPR000051; SAM_Bind.
DR Pfam; PF01189; NOL1_NOP2_Fmu; 1.
DR Pfam; PF01029; NubB; 1.
DR ProDom; PD005242; NubB_region; 1.
DR TIGRFAMs; TIGR00563; rmb; 1.
KM Complete proteome.
SQ SEQUENCE 405 AA; 44708 MW; 89FEC51BB6590C4 CRC64;

Query Match 55.1%; Score 49; DB 2; Length 405;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 10; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 2 PDWLVQMSDRGLD 14
Db 110 PDWLVQMSDRGLD 124

RESULT 4
OSN4J9 SYN6 PRELIMINARY; PRT; 779 AA.
ID OSN4J9 SYN6 PRELIMINARY;
AC OSN4J9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Fremyella diplosiphon (Calothrix PCC 7601).
OC Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Microchaete.
OX NCBI_TaxID=1197;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FDJ3;
RA Stowe-Evans E.L., Ford J., Kehoe D.M.;
RT "Genomic DNA Microarray Analysis: Identification of New Genes
RT Regulated by Light Color in the Cyanobacterium Fremyella
RT diplosiphon.";
RL J. Bacteriol. 186:4338-4349(2004).
RN (2)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FDJ3;
RA Stowe-Evans E., Ford J., Kehoe D.M.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY548438; AAT41885.1; -; Genomic_DNA.
KM Hypothetical protein.
FT NON TER 779
SQ SEQUENCE 779 AA; 85897 MW; 67144DE6E472F0AD CRC64;

Query Match 55.1%; Score 49; DB 2; Length 779;
Best Local Similarity 77.8%; Pred. No. 60;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPDWLMGCD 9
Db 422 EPDWLMGCD 430

RESULT 5
QV3J33 PROMM PRELIMINARY; PRT; 217 AA.
ID QV3J33 PROMM PRELIMINARY;
AC QV3J33;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein precursor.
GN OrderedLocustNames=PMT2247;
OC Prochlorococcus marinus (strain MIT 9313).
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=74547;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA Roca G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation.";
RL Nature 424:1042-1047(2003).
DR EMBL; BX572101; CA822421.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:004605; F:phosphatidate cytidyltransferase activity; IEA.
DR GO; GO:0008654; F:phospholipid biosynthesis; IEA.
DR InterPro; IPR00374; PC_trans.
DR Pfam; PF01148; CTP_transf_1; 1.
KM Complete proteome; Hypothetical protein; Signal.
FT SIGNAL 21
FT SIGNAL 1
SQ SEQUENCE 217 AA; 23832 MW; 522AA449E4033FEC CRC64;

Query Match 53.9%; Score 48; DB 2; Length 217;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PDWLVQMSDRGL 13
Db 139 PDWLVQMSDRGL 150

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RESULT 6

Q8BJF9 SHEON PRELIMINARY; PRT; 262 AA.

ID Q8BJF9

DT 01-MAR-2003 (TReMBLrel. 23, Created)

DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

DE Hypothetical protein S00508.

GN Ordered locus names S00508;

OS Shewanella oneidensis.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;

OC Shewanellaceae; Shewanella.

OX NCBI_TaxID=70863;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=NR-1;

RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;

RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,

RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Melne B.A.,

RA Clayton R.A., Meyer T., Tsapin A., Scott J., Beaman M.J.,

RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,

RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,

RA Lee K., Berry K.J., Lee C., Mueller J., Kouri H.W., Gill J.,

RA Venter J.C., Neilson K.H., Frazer C.M.;

RA "Genome sequence of the dissimilatory metal ion-reducing bacterium

RT Shewanella oneidensis."

RL Nat. Biotechnol. 20:1118-1123(2002).

DR EMBL; AF015498; AAN53589.1; -; Genomic_DNA.

DR TIGR; S00508; -;

KM Complete proteome.

SQ SEQUENCE 262 AA; 29556 MW; 5E5B6F4D52DC44C CRC64;

Query Match 53.9%; Score 48; DB 2; Length 262;

Best Local Similarity 61.5%; Pred. No. 29;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 PDMLMGDRGALD 14

DB 58 PDMLMGDRGALD 70

RESULT 7

Q5SSSO CRYNE PRELIMINARY; PRT; 426 AA.

ID Q5SSSO

DT 13-SEP-2005 (TReMBLrel. 31, Created)

DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)

DE Hypothetical protein.

GN ORFNames=CNBE1140;

OS Cryococcus neoformans var. neoformans B-3501A.

OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;

OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.

OX NCBI_TaxID=283643;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=B-3501A;

RX Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,

RA Wicks B.L., Fu J., Davis R.W.;

RT "Cryococcus neoformans serotype D sequencing."

RT Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

CC -1- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

CC EMBL; AAEY0100024; EAL20751.1; -; Genomic_DNA.

KM Hypothetical protein.

SQ SEQUENCE 426 AA; 47024 MW; A0FBD1F268A28310 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 426;

Best Local Similarity 53.3%; Pred. No. 47;

Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EPDMLMGDRGALD 15

DB 328 EPDMLMGDRGALD 342

RESULT 8

Q9S4Z3 SALEN PRELIMINARY; PRT; 448 AA.

ID Q9S4Z3

DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE Hypothetical protein (Fragment).

OS Salmonella enteritidis.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Salmonella.

OX NCBI_TaxID=592;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=S1400;

RX MEDLINE=99377131; PubMed=10447888;

RA Paterly T., Hernalsteens J.-P., De Greve H.;

RA "Identification and molecular characterization of a novel Salmonella

RT enteritidis pathogenicity islet encoding an ABC transporter."

RT Mol. Microbiol. 33:791-805(1999).

DR EMBL; AF102556; AAD51877.1; -; Genomic_DNA.

DR GO; GO:0016020; C:membrane; IEA.

DR InterPro; IPR003838; DUF214.

DR Pfam; PF02687; FtsX; 1.

KM Hypothetical protein.

FT NON TER 1

SQ SEQUENCE 448 AA; 49706 MW; 389077E50235C42A CRC64;

Query Match 53.9%; Score 48; DB 2; Length 448;

Best Local Similarity 87.5%; Pred. No. 49;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EPDMLMG 8

DB 408 EPDMLMG 415

RESULT 9

Q59SA1 CANAL PRELIMINARY; PRT; 775 AA.

ID Q59SA1

DT 10-MAY-2005 (TReMBLrel. 30, Created)

DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)

DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)

DE Hypothetical protein.

GN ORFNames=CaO19.10974;

OS Candida albicans SC5314.

OC Eukaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycetes;

OC Saccharomycetales; mltosporic Saccharomycetales; Candida.

OX NCBI_TaxID=237561;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=SC5314;

RX PubMed=15133810; DOI=10.1073/pnas.0401648101;

RA Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,

RA Magee B.B., Newport G., Thorstensen Y.R., Agabian N., Magee P.T.,

RA Davis R.W., Scherer S.;

RT "The diploid genome sequence of Candida albicans."

RT Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=SC5314;

RX Dungan J., Cuo A., Newport G., Ian C.-Y., Iijima C., Adegoke O.,

RA Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,

RA Jones T., Scherer S., Agabian N.;

RT "Annotation of the Genome of *Candida albicans*.";
RL Submitted (Apr-2004) to the EMBL/Genbank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AAC00100154; EAK93359.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 775 AA; 88474 MW; 685118C6B2C914A8 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 775;
Best Local Similarity 54.5%; Pred. No. 86;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 PDWLMGDRGA 12
DB 718 PEMAVMGSGGA 728

RESULT 10
Q8GM13 STRCL PRELIMINARY; PRT; 784 AA.
AC Q8GM13-
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE UvrA-like drug resistance pump.
OS Streptomyces globisporus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycetaceae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxId=1908;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22171413; PubMed=12183628; DOI=10.1126/science.1072110;
RA Liu W., Christensen S.D., Standage S., Shen B.,
RT "Biosynthesis of the enediyne antitumor antibiotic C-1027.";
SC Science 297:1170-1173(2002).
CC -! SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AY048670; AAL06654.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro: IPR003439; ABC transp_like.
DR Pfam: PF00005; ABC transp_2.
DR PROSITE: PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE: PS00893; ABC_TRANSPORTER_2; 2.
KW ATP-binding; Membrane; Nucleotide-binding; Transport.
SQ SEQUENCE 784 AA; 83960 MW; DABCD2D965720A5E7 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 784;
Best Local Similarity 53.8%; Pred. No. 87;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 PDWLMGDRGALD 14
DB 204 PDMQIMAKSGRLD 216

RESULT 11
Q59870 CANAL PRELIMINARY; PRT; 793 AA.
AC Q59870-
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=CaO19.3470;
OS *Candida albicans* SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; *Candida*.
OX NCBI_TaxId=237561;

RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federle N.A., Chibana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.
RT "The diploid genome sequence of *Candida albicans*.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dungan J., Kuo A., Newport G., Ian C.-Y., Iijima C., Adegoke O.,
RA Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
RA Jones T., Scherer S., Agabian N.
RT "Annotation of the Genome of *Candida albicans*.";
RL Submitted (Apr-2004) to the EMBL/Genbank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AAC00100155; EAK93328.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 793 AA; 90808 MW; 870A0A0508ADFB27 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 793;
Best Local Similarity 54.5%; Pred. No. 88;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 PDWLMGDRGA 12
DB 735 PEMAVMGSGGA 745

RESULT 12
Q8ZR90 SALTY PRELIMINARY; PRT; 804 AA.
AC Q8ZR90-
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Putative inner membrane protein.
GN Name=ybbp; OrderedLocNames=STW0508;
OS *Salmonella typhimurium*.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; *Salmonella*.
OX NCBI_TaxId=602;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=LT2;
RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porrolik S., Ail J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.
RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
LT2.";
RL Nature 413:852-856(2001).
DR EMBL; AE008719; AAL19462.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro: IPR003838; DUF214.
DR Pfam: PF02687; Ptex; 2.
KW Complete proteome.
SQ SEQUENCE 804 AA; 88772 MW; 72A29069A7021F11 CRC64;

Query Match 53.9%; Score 48; DB 2; Length 804;
Best Local Similarity 87.5%; Pred. No. 89;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EPDWLMG 8
DB 764 EPDWRLMG 771

Query Match 53.9%; Score 48; DB 2; Length 793;
Best Local Similarity 54.5%; Pred. No. 88;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 PDWLMGDRGA 12
DB 735 PEMAVMGSGGA 745

RESULT 12
Q8ZR90 SALTY PRELIMINARY; PRT; 804 AA.
AC Q8ZR90-
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Putative inner membrane protein.
GN Name=ybbp; OrderedLocNames=STW0508;
OS *Salmonella typhimurium*.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; *Salmonella*.
OX NCBI_TaxId=602;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=LT2;
RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porrolik S., Ail J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.
RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
LT2.";
RL Nature 413:852-856(2001).
DR EMBL; AE008719; AAL19462.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro: IPR003838; DUF214.
DR Pfam: PF02687; Ptex; 2.
KW Complete proteome.
SQ SEQUENCE 804 AA; 88772 MW; 72A29069A7021F11 CRC64;

RESULT 15	
Q7UG34_RHOBA	
ID Q7UG34_RHOBA PRELIMINARY;	PRT; 364 AA
AC Q7UG34;	

Search completed: December 4, 2005, 04:52:25
Job time : 139.875 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 03:59:51 ; Search time 32.1875 Seconds
(without alignments)
38.528 Million cell updates/sec

Title: US-10-632-706-197

Perfect score: 89
Sequence: 1 EPPDWLIMGDRGALDV 15Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Parents AA:
1: /cgn2_6/prodata/1/aa/5.COMB.pep.*
2: /cgn2_6/prodata/1/aa/6.COMB.pep.*
3: /cgn2_6/prodata/1/aa/H.COMB.pep.*
4: /cgn2_6/prodata/1/aa/PCTUS.COMB.pep.*
5: /cgn2_6/prodata/1/aa/RE.COMB.pep.*
6: /cgn2_6/prodata/1/aa/backfileall.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	48	53.9	229	2	US-09-489-039A-12532	Sequence 12532, A
2	45	50.6	614	2	US-09-543-681A-7066	Sequence 7066, Ap
3	44	49.4	80	2	US-09-248-796A-22630	Sequence 22630, A
4	43	48.3	345	2	US-09-303-518D-194	Sequence 194, App
5	43	48.3	383	2	US-09-303-518D-196	Sequence 196, App
6	43	48.3	638	2	US-09-949-016-9984	Sequence 9984, Ap
7	43	48.3	732	2	US-09-902-540-13627	Sequence 13627, A
8	42.5	47.8	320	2	US-09-252-991A-18301	Sequence 18301, A
9	42	47.2	174	2	US-09-854-133-426	Sequence 426, App
10	42	47.2	388	1	US-08-290-448A-80	Sequence 80, App
11	42	47.2	388	1	US-08-290-448A-80	Sequence 80, App
12	42	47.2	388	1	US-08-175-069A-80	Sequence 80, App
13	42	47.2	388	2	US-08-461-939B-80	Sequence 80, App
14	42	47.2	388	2	US-08-464-000-80	Sequence 80, App
15	42	47.2	493	2	US-09-489-039A-12903	Sequence 12903, A
16	41	46.1	588	1	PCT-US95-13749-4	Sequence 4, App
17	41	46.1	611	2	US-09-543-681A-7786	Sequence 7786, Ap
18	41	46.1	884	2	US-09-248-796A-20574	Sequence 20574, A
19	40.5	45.5	488	2	US-08-311-731A-29	Sequence 29, App
20	40	44.9	392	2	US-08-252-991A-27798	Sequence 27798, A
21	40	44.9	497	2	US-09-489-039A-12027	Sequence 12027, A
22	40	44.9	576	2	US-09-367-206-1	Sequence 1, App
23	40	44.9	576	2	US-09-367-206-21	Sequence 21, App
24	40	44.9	576	2	US-09-367-206-22	Sequence 22, App
25	40	44.9	576	2	US-09-367-206-23	Sequence 23, App
26	40	44.9	576	2	US-09-298-404-1	Sequence 1, App
27	40	44.9	576	2	US-09-298-404-21	Sequence 21, App

28	40	44.9	576	2	US-09-298-404-22	Sequence 22, App
29	40	44.9	576	2	US-09-298-404-23	Sequence 23, App
30	40	44.9	776	2	US-09-165-396-3	Sequence 3, App
31	39	43.8	13	1	US-08-321-625-44	Sequence 44, App
32	39	43.8	13	2	US-09-181-083-44	Sequence 44, App
33	39	43.8	13	2	US-09-750-754-44	Sequence 44, App
34	39	43.8	93	2	US-09-072-596-272	Sequence 272, App
35	39	43.8	93	2	US-09-072-596-277	Sequence 277, App
36	39	43.8	93	2	US-10-193-002-272	Sequence 272, App
37	39	43.8	93	2	US-10-084-843-277	Sequence 277, App
38	39	43.8	141	2	US-09-902-540-14417	Sequence 14417, A
39	39	43.8	170	2	US-09-270-767-45277	Sequence 45277, A
40	39	43.8	194	2	US-09-489-039A-7558	Sequence 7558, Ap
41	39	43.8	226	2	US-09-004-731-8	Sequence 8, App
42	39	43.8	226	2	US-08-749-699-8	Sequence 8, App
43	39	43.8	226	2	US-09-004-729-8	Sequence 8, App
44	39	43.8	258	2	US-09-134-000C-5594	Sequence 5594, Ap
45	39	43.8	286	2	US-09-248-796A-23020	Sequence 23020, A

ALIGNMENTS

```
RESULT 1
US-09-489-039A-12532
Sequence 12532, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12532
LENGTH: 229
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12532

Query Match      53.9%; Score 48; DB 2; Length 229;
Best Local Similarity 57.1%; Pred. No. 7.8;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      1 EPPDWLIMGDRGALD 14
Db      32 ERSWCKMGDRFAID 45

RESULT 2
US-09-543-681A-7066
Sequence 7066, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7066
LENGTH: 614
TYPE: PRT
ORGANISM: Proteus mirabilis
US-09-543-681A-7066

Query Match      50.6%; Score 45; DB 2; Length 614;
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Best Local Similarity 64.3%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPDWLMGDRGALD 14
DB 452 EDGWLRTGDAGALD 465

RESULT 3

US-09-248-796A-22630
; Sequence 22630, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 22630
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-22630

Query Match 49.4%; Score 44; DB 2; Length 80;
Best Local Similarity 54.5%; Pred. No. 10;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 PDWLMGDRGA 12
DB 12 PDMAVWGQMA 22

RESULT 4

US-09-303-518D-194
; Sequence 194, Application US/09303518D
; Patent No. 6914131
; GENERAL INFORMATION:
; APPLICANT: Scariato, Vincenzo
; APPLICANT: Maignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Neisserial Antigens
; FILE REFERENCE: CHIR0160
; CURRENT APPLICATION NUMBER: US/09/303,518D
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1098
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 194
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-09-303-518D-194

Query Match 48.3%; Score 43; DB 2; Length 345;
Best Local Similarity 70.0%; Pred. No. 72;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PDWLMGDRG 11
DB 183 PEMLFGYRG 192

RESULT 5

US-09-303-518D-196
; Sequence 196, Application US/09303518D

; Patent No. 6914131
; GENERAL INFORMATION:
; APPLICANT: Scariato, Vincenzo
; APPLICANT: Maignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Neisserial Antigens
; FILE REFERENCE: CHIR0160
; CURRENT APPLICATION NUMBER: US/09/303,518D
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1098
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 196
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-303-518D-196

Query Match 48.3%; Score 43; DB 2; Length 383;
Best Local Similarity 70.0%; Pred. No. 81;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PDWLMGDRG 11
DB 181 PEMLFGYRG 190

RESULT 6

US-09-949-016-9984
; Sequence 9984, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9984
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9984

Query Match 48.3%; Score 43; DB 2; Length 638;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EPDWLM 7
DB 558 EPDWLTM 564

RESULT 7

US-09-902-540-13627
; Sequence 13627, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 13627

LENGTH: 732

TYPE: PRT

ORGANISM: Myxococcus xanthus

US-09-902-540-13627

Query Match 48.3%; Score 43; DB 2; Length 732;
Best Local Similarity 63.6%; Pred. No. 1.6e+02;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 4 WLMGDRGALD 14
126 WLMGTRRAAE 136

RESULT 8

US-09-252-991A-18301

Sequence 18301, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 18301

LENGTH: 320

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-18301

Query Match 47.8%; Score 42.5; DB 2; Length 320;
Best Local Similarity 66.7%; Pred. No. 79;

Matches 10; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 2 PDMWLGDRG-ALDV 15
Db 254 PTLWLGDRDRVLDV 268

RESULT 9

US-09-854-133-426

Sequence 426, Application US/09854133

Patent No. 6759308

GENERAL INFORMATION:

APPLICANT: Lodes, Michael J.

APPLICANT: Mohamath, Raodoh

APPLICANT: Henderson, Robert A.

APPLICANT: Benson, Darin R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

FILE REFERENCE: 210121.475C10

CURRENT APPLICATION NUMBER: US/09/854,133

PRIOR FILING DATE: 2001-05-11

NUMBER OF SEQ ID NOS: 735

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 426

LENGTH: 174

TYPE: PRT

ORGANISM: Homo sapiens

US-09-854-133-426

Query Match 47.2%; Score 42; DB 2; Length 174;

Best Local Similarity 70.0%; Pred. No. 49;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EPDMWLGDR 10
Db 124 DPGHLMGDR 133

RESULT 10

US-08-290-448A-80

Sequence 80, Application US/08290448A

Patent No. 5676954

GENERAL INFORMATION:

APPLICANT: Rogers, Bruce

APPLICANT: Klapper, David G.

APPLICANT: Rafnar, Thorunn

APPLICANT: Kuo, Mei-chang

TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses

NUMBER OF SEQUENCES: 93

CORRESPONDENCE ADDRESS:

STREET: 60 State Street, suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/290,448A

FILING DATE: August 15, 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/529,951

FILING DATE: May 29, 1990

APPLICATION NUMBER: US 07/325,365

FILING DATE: March 17, 1989

ATTORNEY/AGENT INFORMATION:

NAME: Amy E. Mandragouras

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: IMI-018CN

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 80:

SEQUENCE CHARACTERISTICS:

LENGTH: 388 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-290-448A-80

Query Match 47.2%; Score 42; DB 1; Length 388;

Best Local Similarity 46.7%; Pred. No. 1.2e+02;

Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 EPDMWLGDRGALDV 15
Db 323 EPDMWTWMTQNDV 337

RESULT 11

US-08-290-448A-80

Sequence 80, Application US/08290448A

Patent No. 5698204

GENERAL INFORMATION:

APPLICANT: Rogers, Bruce

APPLICANT: Klapper, David G.

APPLICANT: Rafnar, Thorunn

APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,448A
FILING DATE: August 15, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-290-448A-80

Query Match 47.2%; Score 42; DB 1; Length 388;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EPDWLWGDGALDV 15
||:|:|
Db 323 EPEWMTNMRQNDV 337

RESULT 12
US-08-175-069A-80
Sequence 80, Application US/08175069A
Patent No. 5776761
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Proteins From Ragweed and Uses
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/175,069A
FILING DATE: December 29, 1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/529,951
FILING DATE: May 29, 1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: March 17, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-175-069A-80

Query Match 47.2%; Score 42; DB 1; Length 388;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EPDWLWGDGALDV 15
||:|:|
Db 323 EPEWMTNMRQNDV 337

RESULT 13
US-08-461-939B-80
Sequence 80, Application US/08461939B
Patent No. 6335019
GENERAL INFORMATION:
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Methods For Treating Sensitivity To A
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,939B
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/464,000
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: US 08/290,448
FILING DATE: 15-AUG-1994
APPLICATION NUMBER: US 07/529,951
FILING DATE: 29-MAY-1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: 17-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CNDV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 80:

SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-939B-80

Query Match 47.2%; Score 42; DB 2; Length 388;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EPDMLMGDRGALDV 15
Db 323 EPEWMTWNRONDV 337

RESULT 14

US-08-464-000-80
Sequence 80, Application US/08464000

GENERAL INFORMATION:
PATENT No. 6335020
APPLICANT: Rogers, Bruce
APPLICANT: Klapper, David G.
APPLICANT: Rafnar, Thorunn
APPLICANT: Kuo, Mei-chang
TITLE OF INVENTION: Allergenic Peptides from Ragweed Pollen
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,000
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/290,448
FILING DATE: 15-AUG-1994
APPLICATION NUMBER: US 07/529,951
FILING DATE: 29-MAY-1990
APPLICATION NUMBER: US 07/325,365
FILING DATE: 17-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-018CN2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-000-80

Query Match 47.2%; Score 42; DB 2; Length 388;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EPDMLMGDRGALDV 15
Db 323 EPEWMTWNRONDV 337

RESULT 15
US-09-489-039A-12903
Sequence 12903, Application US/09489039A

GENERAL INFORMATION:
PATENT No. 6610836
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT FILING DATE: 2000-01-27
CURRENT APPLICATION NUMBER: US/09/489,039A
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12903
LENGTH: 493
TYPE: PRN
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12903

Query Match 47.2%; Score 42; DB 2; Length 493;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 WLLMGDRGL 13
Db 463 WLLMCEGVM 472

Search completed: December 4, 2005, 04:09:44
Job time : 33.1875 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:07:28 ; Search time 107.5 Seconds
(without alignments)
58.302 Million cell updates/sec

Title: US-10-632-706-197

Perfect score: 89

Sequence: 1 EPPDWLMGDRGALDV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications_AA_Main:*
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2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
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6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	89	100.0	15	US-10-632-706-129	Sequence 129, App
2	89	100.0	15	US-10-632-706-130	Sequence 130, App
3	89	100.0	15	US-10-632-706-131	Sequence 131, App
4	89	100.0	15	US-10-632-706-194	Sequence 194, App
5	89	100.0	15	US-10-632-706-197	Sequence 197, App
6	89	100.0	15	US-10-632-706-200	Sequence 200, App
7	75	84.3	15	US-10-632-706-203	Sequence 203, App
8	51	57.3	334	US-10-450-763-50690	Sequence 50690, A
9	48	53.9	201	US-10-634-548-27	Sequence 27, Appl
10	48	53.9	775	US-10-159-257A-160	Sequence 160, App
11	47.5	53.4	992	US-10-437-963-134365	Sequence 134365, A
12	47	52.8	455	US-10-450-763-52883	Sequence 52883, A
13	47	52.8	904	US-10-369-493-12420	Sequence 12420, A
14	45	50.6	159	US-10-425-115-240160	Sequence 240160, A
15	45	50.6	372	US-10-282-122A-66332	Sequence 66332, A
16	44.5	50.0	203	US-10-767-701-42189	Sequence 42189, A
17	44.5	50.0	394	US-10-425-115-243524	Sequence 243524, A
18	44	49.4	472	US-10-617-161-1674	Sequence 1674, Ap
19	44	49.4	472	US-10-392-798-11334	Sequence 11334, Ap
20	44	49.4	505	US-10-437-963-179634	Sequence 179634, A
21	44	49.4	687	US-10-369-493-20876	Sequence 20876, A
22	43.5	48.9	77	US-10-425-115-263892	Sequence 263892, A
23	43	48.3	264	US-10-156-761-11420	Sequence 11420, A
24	43	48.3	368	US-10-437-963-115853	Sequence 115853, A
25	43	48.3	439	US-10-156-761-13497	Sequence 13497, A
26	43	48.3	616	US-10-808-522-8	Sequence 8, Appl
27	43	48.3	1975	US-10-437-963-140079	Sequence 140079, A

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28	42.5	47.8	315	4	US-10-282-122A-43588	Sequence 43588, A
29	42	47.2	77	3	US-09-764-847-922	Sequence 922, App
30	42	47.2	77	4	US-10-092-154-922	Sequence 922, App
31	42	47.2	116	4	US-10-424-599-206981	Sequence 206981, A
32	42	47.2	131	3	US-09-864-408A-4566	Sequence 4566, Ap
33	42	47.2	154	4	US-10-312-354-26	Sequence 26, Appl
34	42	47.2	174	3	US-09-738-973-426	Sequence 426, App
35	42	47.2	174	3	US-09-854-133-426	Sequence 426, App
36	42	47.2	174	3	US-10-144-649A-426	Sequence 426, App
37	42	47.2	175	5	US-10-450-763-31629	Sequence 31629, A
38	42	47.2	198	4	US-10-767-701-34131	Sequence 34131, A
39	42	47.2	211	5	US-10-450-763-37978	Sequence 37978, A
40	42	47.2	245	4	US-10-437-963-108592	Sequence 108592, A
41	42	47.2	275	4	US-10-425-114-66625	Sequence 66625, A
42	42	47.2	363	4	US-10-282-122A-50322	Sequence 50322, A
43	42	47.2	380	4	US-10-369-493-20944	Sequence 20944, A
44	42	47.2	397	3	US-09-847-208-17	Sequence 17, Appl
45	42	47.2	397	5	US-10-809-689-97	Sequence 97, Appl

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RESULT 1
US-10-632-706-129
; Sequence 129, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 40/T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 129
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: single chain antibody fragment
US-10-632-706-129

Query Match      100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 EPPDWLMGDRGALDV 15
Db      1 EPPDWLMGDRGALDV 15

RESULT 2
US-10-632-706-130
; Sequence 130, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
; APPLICANT: AMERSDORFER, PETER
; TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
; FILE REFERENCE: 40/T-895120US
; CURRENT APPLICATION NUMBER: US/10/632,706
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US 60/400,721
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US 09/144,806

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/ PRIOR FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 278
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 130
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: single chain antibody fragment
US-10-632-706-130

Query Match 100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDWLWMDRGALDV 15
DB 1 EPDWLWMDRGALDV 15

RESULT 3
US-10-632-706-131
/ Sequence 131, Application US/10632706
/ Publication No. US20040175385A1
/ GENERAL INFORMATION:
/ APPLICANT: MARKS, JAMES D.
/ APPLICANT: AMERSDORFER, PETER
/ TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
/ FILE REFERENCE: 407T-895120US
/ CURRENT APPLICATION NUMBER: US/10/632,706
/ PRIOR FILING DATE: 2003-08-01
/ PRIOR APPLICATION NUMBER: US 60/400,721
/ PRIOR FILING DATE: 2002-08-01
/ PRIOR FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 278
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 131
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: single chain antibody fragment
US-10-632-706-131

Query Match 100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDWLWMDRGALDV 15
DB 1 EPDWLWMDRGALDV 15

RESULT 4
US-10-632-706-194
/ Sequence 194, Application US/10632706
/ Publication No. US20040175385A1
/ GENERAL INFORMATION:
/ APPLICANT: MARKS, JAMES D.
/ APPLICANT: AMERSDORFER, PETER
/ TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
/ FILE REFERENCE: 407T-895120US
/ CURRENT APPLICATION NUMBER: US/10/632,706
/ PRIOR FILING DATE: 2003-08-01
/ PRIOR APPLICATION NUMBER: US 60/400,721
/ PRIOR FILING DATE: 2002-08-01
/ PRIOR APPLICATION NUMBER: US 09/144,806
/ PRIOR FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 278
/ SOFTWARE: Patentin version 3.2

/ SEQ ID NO 194
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: single chain antibody fragment
US-10-632-706-194

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Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDWLWMDRGALDV 15
DB 1 EPDWLWMDRGALDV 15

RESULT 5
US-10-632-706-197
/ Sequence 197, Application US/10632706
/ Publication No. US20040175385A1
/ GENERAL INFORMATION:
/ APPLICANT: MARKS, JAMES D.
/ APPLICANT: AMERSDORFER, PETER
/ TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
/ FILE REFERENCE: 407T-895120US
/ CURRENT APPLICATION NUMBER: US/10/632,706
/ PRIOR FILING DATE: 2003-08-01
/ PRIOR APPLICATION NUMBER: US 60/400,721
/ PRIOR FILING DATE: 2002-08-01
/ PRIOR APPLICATION NUMBER: US 09/144,806
/ PRIOR FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 278
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 197
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: single chain antibody fragment
US-10-632-706-197

Query Match 100.0%; Score 89; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPDWLWMDRGALDV 15
DB 1 EPDWLWMDRGALDV 15

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US-10-632-706-200
/ Sequence 200, Application US/10632706
/ Publication No. US20040175385A1
/ GENERAL INFORMATION:
/ APPLICANT: MARKS, JAMES D.
/ APPLICANT: AMERSDORFER, PETER
/ TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
/ FILE REFERENCE: 407T-895120US
/ CURRENT APPLICATION NUMBER: US/10/632,706
/ PRIOR FILING DATE: 2003-08-01
/ PRIOR APPLICATION NUMBER: US 60/400,721
/ PRIOR FILING DATE: 2002-08-01
/ PRIOR APPLICATION NUMBER: US 09/144,806
/ PRIOR FILING DATE: 1998-08-31
/ NUMBER OF SEQ ID NOS: 278
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 200
/ LENGTH: 15
/ TYPE: PRT


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/ TITLE OF INVENTION: ANTIBIOTIC C-1027
/ FILE REFERENCE: 4077-896020US
/ CURRENT APPLICATION NUMBER: US/10/159,257A
/ PRIOR FILING DATE: 2002-05-31
/ PRIOR APPLICATION NUMBER: 09/478,188
/ PRIOR FILING DATE: 2000-01-05
/ PRIOR APPLICATION NUMBER: 60/115,434
/ PRIOR FILING DATE: 1999-01-06
/ NUMBER OF SEQ ID NOS: 207
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 160
/ LENGTH: 775
/ TYPE: PRT
/ ORGANISM: Streptomyces globisporus
/ FEATURE:
/ OTHER INFORMATION: orf(-1)
US-10-159-257A-160

Query Match          53.9%; Score 48; DB 4; Length 775;
Best Local Similarity 53.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      2 PDWLMGDRGALD 14
DB      195 PDWQIMAKSGRLD 207

RESULT 11
US-10-437-963-134365
/ Sequence 134365, Application US/10437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boulharov, Andrey A.
/ APPLICANT: Bardazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
/ TITLE OF INVENTION: Plants and Uses thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO: 134365
/ LENGTH: 992
/ TYPE: PRT
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_36146C.1.pep
US-10-437-963-134365

Query Match          53.4%; Score 47.5; DB 4; Length 992;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY      1 EPDWL---MGDRGALDY 15
DB      551 EPNWLDWYWGDKGTGTV 568

RESULT 12
US-10-450-763-52883
/ Sequence 52883, Application US/10450763
/ Publication No. US20050196754A1
/ GENERAL INFORMATION:
/ APPLICANT: HySeq, Inc
/ TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
/ FILE REFERENCE: 790CIP3/US
/ CURRENT APPLICATION NUMBER: US/10/450,763
/ CURRENT FILING DATE: 2003-06-11
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/ PRIOR APPLICATION NUMBER: PCT/US01/08631
/ PRIOR FILING DATE: 2001-03-30
/ PRIOR APPLICATION NUMBER: 09/540,217
/ PRIOR FILING DATE: 2000-03-31
/ PRIOR APPLICATION NUMBER: 09/649,167
/ PRIOR FILING DATE: 2000-08-23
/ NUMBER OF SEQ ID NOS: 60736
/ SOFTWARE: Custom
/ SEQ ID NO: 52883
/ LENGTH: 455
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)...(455)
/ OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-52883

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Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1 EPDWLMGDRGAL 13
DB      93 EONWLMCERGVM 105

RESULT 13
US-10-369-493-12420
/ Sequence 12420, Application US/10369493
/ Publication No. US20030233675A1
/ GENERAL INFORMATION:
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Hinkle, Gregory J.
/ APPLICANT: Slater, Steven C.
/ APPLICANT: Goldman, Barry S.
/ APPLICANT: Chen, Xianfeng
/ TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
/ FILE REFERENCE: 38-10(52052)B
/ CURRENT APPLICATION NUMBER: US/10/369,493
/ CURRENT FILING DATE: 2003-02-28
/ PRIOR APPLICATION NUMBER: US 60/360,039
/ PRIOR FILING DATE: 2002-02-21
/ NUMBER OF SEQ ID NOS: 47374
/ SEQ ID NO: 12420
/ LENGTH: 904
/ TYPE: PRT
/ ORGANISM: Aspergillus nidulans
US-10-369-493-12420

Query Match          52.8%; Score 47; DB 4; Length 904;
Best Local Similarity 70.0%; Pred. No. 2.1e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      4 WLWMDRGAL 13
DB      460 WLWMDKTSL 469

RESULT 14
US-10-425-115-240160
/ Sequence 240160, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
/ TITLE OF INVENTION: Plants
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
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; CURRENT FILING DATE: 2003-04-28
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; SEQ ID NO 240160
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Zee mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(159)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_150607C.1.pap
US-10-425-115-240160

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Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB      35 PGRLMGRRGAL 46

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RESULT 15
US-10-282-122A-68332
; Sequence 68332, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangau
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68332
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Pseudomonas putida
US-10-282-122A-68332

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Query Match      50.6%; Score 45; DB 4; Length 372;
Best Local Similarity 70.0%; Pred. No. 1,86+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB      221 PDMLMTPAG 230

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GenCore version 5.1.6
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Run on: December 4, 2005, 04:08:08 ; Search time 4.375 Seconds
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16.417 Million cell updates/sec

Title: US-10-632-706-197
Perfect score: 89
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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0
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Post-Processing: Minimum Match 0%
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8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	43	48.3	383	6 US-10-467-657-5602	Sequence 5602, Ap
2	41	46.1	251	7 US-11-054-515-1084	Sequence 1084, Ap
3	40.5	45.5	125	6 US-10-821-234-1277	Sequence 1277, Ap
4	38.5	43.3	1075	7 US-11-174-150-34	Sequence 34, Appl
5	38.5	43.3	1114	7 US-11-174-150-35	Sequence 35, Appl
6	38	42.7	248	7 US-11-054-515-1679	Sequence 1679, Ap
7	38	42.7	251	7 US-11-054-515-944	Sequence 944, Appl
8	37	41.6	344	6 US-10-967-527A-24	Sequence 24, Appl
9	36	40.4	225	6 US-10-821-234-1116	Sequence 1116, Ap
10	36	40.4	322	6 US-10-467-657-1006	Sequence 1006, Ap
11	36	40.4	428	6 US-10-793-626-484	Sequence 484, Appl
12	36	40.4	1857	7 US-11-057-058-60	Sequence 60, Appl
13	36	40.4	1857	7 US-11-057-058-61	Sequence 61, Appl
14	35.5	39.9	158	6 US-10-510-386-128	Sequence 128, Appl
15	35.5	39.9	247	6 US-10-793-626-1466	Sequence 1466, Ap
16	35.5	39.9	344	6 US-10-821-234-923	Sequence 923, Appl
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18	35	39.3	229	6 US-10-957-659-54	Sequence 54, Appl
19	35	39.3	350	6 US-10-467-657-5824	Sequence 5824, Ap
20	35	39.3	401	6 US-10-510-386-68	Sequence 68, Appl
21	35	39.3	530	6 US-10-980-388-62	Sequence 62, Appl
22	35	39.3	551	6 US-10-793-626-1668	Sequence 1668, Ap
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24	34.5	38.8	1613	7 US-11-108-528-86	Sequence 86, Appl
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26	34	38.2	251	7 US-11-054-515-1793	Sequence 1793, Ap
27	34	38.2	253	7 US-11-015-546A-2	Sequence 2, Appl
28	34	38.2	253	7 US-11-054-515-1069	Sequence 1069, Ap
29	34	38.2	269	7 US-11-015-546A-10	Sequence 10, Appl
30	34	38.2	274	7 US-11-015-546A-12	Sequence 12, Appl
31	34	38.2	486	6 US-10-821-234-1063	Sequence 1063, Ap
32	34	38.2	613	6 US-10-131-826A-190	Sequence 190, Appl
33	34	38.2	613	6 US-10-131-826A-206	Sequence 206, Appl
34	34	38.2	820	7 US-11-147-047-31	Sequence 31, Appl
35	34	38.2	2725	7 US-11-113-424-52	Sequence 52, Appl
36	33.5	37.6	137	6 US-10-821-234-882	Sequence 882, Appl
37	33.5	37.6	249	7 US-11-054-515-649	Sequence 649, Appl
38	33	37.1	91	6 US-10-467-657-1052	Sequence 1052, Ap
39	33	37.1	177	6 US-10-980-388-95	Sequence 95, Appl
40	33	37.1	247	7 US-11-054-515-1307	Sequence 1307, Ap
41	33	37.1	248	7 US-11-054-515-877	Sequence 877, Appl
42	33	37.1	248	7 US-11-054-515-953	Sequence 953, Appl
43	33	37.1	248	7 US-11-054-515-965	Sequence 965, Appl
44	33	37.1	248	7 US-11-054-515-980	Sequence 980, Appl
45	33	37.1	248	7 US-11-054-515-984	Sequence 984, Appl

ALIGNMENTS

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RESULT 1
US-10-467-657-5602
; Sequence 5602, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5602
; LENGTH: 383
; TYPE: PRP
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5602

Query Match      48.3%; Score 43; DB 6; Length 383;
Best Local Similarity 70.0%; Pred. No. 3.8;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 PPDMLMGDRG 11
      |:|:|:|:|
DB      181 PPDMLMGDRG 190

RESULT 2
US-11-054-515-1084
; Sequence 1084, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunoselectively Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
```

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/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 1084
/ LENGTH: 251
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-1084
```

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Query Match          46.1%; Score 41; DB 7; Length 251;
Best Local Similarity 46.2%; Pred. No. 5.1;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      2 PDWLWMDRGALD 14
DB      45 PEMWGMINGRGS 57
```

```
RESULT 3
US-10-821-234-1277
/ Sequence 1277, Application US/10821234
/ Publication No. US20050255114A1
/ GENERAL INFORMATION:
/ APPLICANT: Labac, Ivan
/ APPLICANT: Stache-Crain, Birgit
/ APPLICANT: Andarmati, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Method for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ CURRENT FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pc_seq_genes Version 1.0
/ SEQ ID NO 1277
/ LENGTH: 125
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-821-234-1277
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Query Match          45.5%; Score 40.5; DB 6; Length 125;
Best Local Similarity 63.6%; Pred. No. 3.1;
Matches 7; Conservative 3; Mismatches 0; Indels 1; Gaps 1;
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```
OY      1 EPDWLWMDRG 11
DB      101 DDDWLI-GERG 110
```

```
RESULT 4
US-11-174-150-34
/ Sequence 34, Application US/11174150
/ Publication No. US20050260714A1
/ GENERAL INFORMATION:
/ APPLICANT: Agarwal, Pankaj
/ APPLICANT: Murdoch, Paul R.
/ APPLICANT: Rizvi, Safia K.
/ APPLICANT: Smith, Randall F.
```

```
/ APPLICANT: Xiang, Zhaoying
/ TITLE OF INVENTION: NOVEL COMPOUNDS
/ FILE REFERENCE: GP50022
/ CURRENT APPLICATION NUMBER: US/11/174,150
/ CURRENT FILING DATE: 2005-07-01
/ PRIOR APPLICATION NUMBER: US/10/257,174
/ PRIOR FILING DATE: 2002-10-10
/ PRIOR APPLICATION NUMBER: PCT/US01/11797
/ PRIOR FILING DATE: 2001-04-11
/ PRIOR APPLICATION NUMBER: 60/196,603
/ PRIOR FILING DATE: 2000-04-13
/ PRIOR APPLICATION NUMBER: 60/199,417
/ PRIOR FILING DATE: 2000-04-24
/ NUMBER OF SEQ ID NOS: 48
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 34
/ LENGTH: 1075
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-174-150-34
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```
Query Match          43.3%; Score 38.5; DB 7; Length 1075;
Best Local Similarity 53.8%; Pred. No. 5.1;
Matches 7; Conservative 2; Mismatches 1; Indels 3; Gaps 1;
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```
OY      3 DWLWLG---DRGA 12
DB      922 EMSVWGSWYDRGA 934
```

```
RESULT 5
US-11-174-150-35
/ Sequence 35, Application US/11174150
/ Publication No. US20050260714A1
/ GENERAL INFORMATION:
/ APPLICANT: Agarwal, Pankaj
/ APPLICANT: Murdoch, Paul R.
/ APPLICANT: Rizvi, Safia K.
/ APPLICANT: Smith, Randall F.
/ APPLICANT: Xiang, Zhaoying
/ TITLE OF INVENTION: NOVEL COMPOUNDS
/ FILE REFERENCE: GP50022
/ CURRENT APPLICATION NUMBER: US/11/174,150
/ CURRENT FILING DATE: 2005-07-01
/ PRIOR APPLICATION NUMBER: US/10/257,174
/ PRIOR FILING DATE: 2002-10-10
/ PRIOR APPLICATION NUMBER: PCT/US01/11797
/ PRIOR FILING DATE: 2001-04-11
/ PRIOR APPLICATION NUMBER: 60/196,603
/ PRIOR FILING DATE: 2000-04-13
/ PRIOR APPLICATION NUMBER: 60/199,417
/ PRIOR FILING DATE: 2000-04-24
/ NUMBER OF SEQ ID NOS: 48
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 35
/ LENGTH: 1114
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-174-150-35
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Query Match          43.3%; Score 38.5; DB 7; Length 1114;
Best Local Similarity 53.8%; Pred. No. 5.3;
Matches 7; Conservative 2; Mismatches 1; Indels 3; Gaps 1;
```

```
OY      3 DWLWLG---DRGA 12
DB      961 EMSVWGSWYDRGA 973
```

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RESULT 6
US-11-054-515-1679
/ Sequence 1679, Application US/11054515
/ Publication No. US2005025532A1
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; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; REMAINING PRIOR APPLICATION DATA REMOVED - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1679
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1679

Query Match          42.7%; Score 38; DB 7; Length 248;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy      1 EPDWLMGDRGALD 14
||:|:|:|:|:|:|
Db      44 EPEWMGWMINGSGD 57

RESULT 7
US-11-054-515-944
; Sequence 944, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
```

```

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 944
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-944

Query Match          42.7%; Score 38; DB 7; Length 251;
Best Local Similarity 42.9%; Pred. No. 15;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy      1 EPDWLMGDRGALD 14
||:|:|:|:|:|:|
Db      44 EPEWMGWMINGSGD 57

RESULT 8
US-10-967-527A-24
; Sequence 24, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Zcnf14, A Tumor Necrosis Factor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 344
; TYPE: PRT
; ORGANISM: mus musculus
US-10-967-527A-24

Query Match          41.6%; Score 37; DB 6; Length 344;
Best Local Similarity 83.3%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 PDWLMW 7
|||
Db      3 PSWLMW 8

RESULT 9
US-10-821-234-1116
; Sequence 1116, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1116
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1116

Query Match          40.4%; Score 36; DB 6; Length 225;
```

Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 WLMGDRG 11
Db 74 WRMGRG 81

RESULT 10

US-10-467-657-1006
; Sequence 1006, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACT Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMin9, version 1.04
; SEQ ID NO 1006
; LENGTH: 322
; TYPE: PRT
; ORGANISM: *Neisseria gonorrhoeae*
US-10-467-657-1006

Query Match 40.4%; Score 36; DB 6; Length 322;
Best Local Similarity 63.6%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PDWLMGDRGA 12
Db 251 PDWLFVLDRSA 261

RESULT 11

US-10-793-626-484
; Sequence 484, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU348005
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 484
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-484

Query Match 40.4%; Score 36; DB 6; Length 428;
Best Local Similarity 62.5%; Pred. No. 50;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 WGDGRGALD 14
Db 333 WGDKGVD 340

RESULT 12
US-11-057-058-60
; Sequence 60, Application US/11057058
; Publication No. US20050244400A1
; GENERAL INFORMATION:
; APPLICANT: Lebowitz, Jonathan
; APPLICANT: Maga, John
; TITLE OF INVENTION: ACID ALPHA-GLUCOSIDASE AND FRAGMENTS THEREOF
; FILE REFERENCE: SW-011
; CURRENT APPLICATION NUMBER: US/11/057,058
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: US 60/543,812
; PRIOR FILING DATE: 2004-02-10
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 60
; LENGTH: 1857
; TYPE: PRT
; ORGANISM: *Homo sapiens*
US-11-057-058-60

Query Match 40.4%; Score 36; DB 7; Length 1857;
Best Local Similarity 45.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 WLMGDRGALD 14
Db 1749 WLFMDGQSID 1759

RESULT 13

US-11-057-058-61
; Sequence 61, Application US/11057058
; Publication No. US20050244400A1
; GENERAL INFORMATION:
; APPLICANT: Lebowitz, Jonathan
; APPLICANT: Maga, John
; TITLE OF INVENTION: ACID ALPHA-GLUCOSIDASE AND FRAGMENTS THEREOF
; FILE REFERENCE: SW-011
; CURRENT APPLICATION NUMBER: US/11/057,058
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: US 60/543,812
; PRIOR FILING DATE: 2004-02-10
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 61
; LENGTH: 1857
; TYPE: PRT
; ORGANISM: *Homo sapiens*
US-11-057-058-61

Query Match 40.4%; Score 36; DB 7; Length 1857;
Best Local Similarity 45.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 WLMGDRGALD 14
Db 1749 WLFMDGQSID 1759

RESULT 14

US-10-510-386-128
; Sequence 128, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386

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; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 128
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-128

```

```

Query Match          39.9%; Score 35.5; DB 6; Length 158;
Best Local Similarity 72.7%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```

```

QY      5 LLM-GDRGALD 14
      | | | | |
Db      65 LYWTGDRGKLD 75

```

```

RESULT 15
US-10-793-626-1466
; Sequence 1466, Application US/107931626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1466
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1466

```

```

Query Match          39.9%; Score 35.5; DB 6; Length 247;
Best Local Similarity 63.6%; Pred. No. 35;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

```

```

QY      4 WL-LMGDRGAL 13
      | | | | |
Db      186 WMNLWGNVGAL 196

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Search completed: December 4, 2005, 04:37:50
Job time : 5.375 secs

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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:09:54 ; Search time 95.5625 Seconds
(without alignments)
50.576 Million cell updates/sec

Title: US-10-632-706-198
Perfect score: 59
Sequence: 1 WGGGRTVTWSS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: _Genesegp21.*
2: genesegp19808.*
3: genesegp19908.*
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5: genesegp20018.*
6: genesegp20028.*
7: genesegp20038.*
8: genesegp20048.*
9: genesegp20058.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	11	2 AAR85166	Aar85166 Human ONS
2	59	100.0	11	2 AAR85166	Aar85166 Human ONS
3	59	100.0	11	4 AAU07452	Aau07452 Synthetic
4	59	100.0	11	5 AAE28561	Aae28561 scFv anti
5	59	100.0	11	5 AAU70517	Aau70517 Mouse hea
6	59	100.0	11	5 AAU70501	Aau70501 Mouse hea
7	59	100.0	11	5 AAU70485	Aau70485 Mouse hea
8	59	100.0	11	5 AAU70477	Aau70477 Mouse hea
9	59	100.0	11	6 ABO10719	Abol10719 Deimunitis
10	59	100.0	11	6 ABR44663	Abrr44663 Murine J4
11	59	100.0	11	7 ABO33904	Abol33904 Anti-GPI-
12	59	100.0	11	7 ADG75671	Adg75671 Peptide O
13	59	100.0	11	8 ADH17960	Adh17960 Human mod
14	59	100.0	11	8 ADH18011	Adh18011 Human mod
15	59	100.0	11	8 ADG90791	Adg90791 Artificial
16	59	100.0	11	8 ADR12645	Adr12645 Mammalian
17	59	100.0	11	8 ADR38796	Adr38796 Mouse hea
18	59	100.0	11	8 ADR38793	Adr38793 Mouse hea
19	59	100.0	11	8 ADR38802	Adr38802 Mouse hea
20	59	100.0	11	8 ADU38799	Adu38799 Mouse hea
21	59	100.0	11	8 ADU38427	Adu38427 Mouse ant
22	59	100.0	11	8 ADU67919	Adu67919 Mouse ant
23	59	100.0	11	9 ADM07403	Adm07403 Heavy cha
24	59	100.0	11	9 ADM07419	Adm07419 Heavy cha

25	59	100.0	11	9 ADM07407	Adm07407 Heavy cha
26	59	100.0	11	9 ADM07423	Adm07423 Heavy cha
27	59	100.0	11	9 ADM07427	Adm07427 Heavy cha
28	59	100.0	11	9 ADM07435	Adm07435 Heavy cha
29	59	100.0	11	9 ADM07439	Adm07439 Heavy cha
30	59	100.0	11	9 ADM07411	Adm07411 Heavy cha
31	59	100.0	11	9 ADM07443	Adm07443 Heavy cha
32	59	100.0	11	9 ADM07451	Adm07451 Heavy cha
33	59	100.0	11	9 ADM07415	Adm07415 Heavy cha
34	59	100.0	11	9 ADM07447	Adm07447 Heavy cha
35	59	100.0	11	9 ADM07431	Adm07431 Heavy cha
36	59	100.0	11	9 ADY31581	Ady31581 Human ant
37	59	100.0	11	9 ADZ35850	Adz35850 Anti-gluc
38	59	100.0	11	9 ADZ83544	Adz83544 CD3 const
39	59	100.0	11	9 ADZ83542	Adz83542 CD3 const
40	59	100.0	11	9 ADZ83545	Adz83545 CD3 const
41	59	100.0	11	9 ADZ83543	Adz83543 CD3 const
42	59	100.0	11	9 AEA21481	Aea21481 Human ant
43	59	100.0	11	9 AEA21445	Aea21445 Human ant
44	59	100.0	11	9 AEA45691	Aea45691 Apolipop
45	59	100.0	11	9 AEA44171	Aea44171 Anti-TPO

ALIGNMENTS

RESULT 1

AAR85166 standard; protein; 11 AA.

XX AAR85166;

DT 18-JAN-1996 (first entry)

DE Human ONS-M21 antibody heavy variable region FR 4.

XX Human; ONS-M21 antibody; heavy variable region; chimeric protein;

KW Framework region; FR 4; medulloblastoma; brain tumour; treatment;

XX diagnosis.

OS Homo sapiens.

XX WO9514041-A1.

XX 26-MAY-1995.

PF 19-OCT-1994; 94WO-JP001763.

XX 19-NOV-1993; 93JP-00291078.

XX (CHUS) CHUGAI SEIYAKU KK.

PI Ohtomo T, Sato K, Tsuchiya M;

DR WPI; 1995-200347/26.

PT Reconstituted antibody against human medulloblastoma cells - contains

XX high proportion of human antibody origin and has low antigenicity.

XX Claim 18; Page 102; 120pp; Japanese.

CC AAR85163-R85166 are human antibody ONS-M21 heavy variable region

CC Framework regions (FRs). They were used in the construction of a

CC human/murine chimeric antibody, reactive with human medulloblastoma (a

CC brain tumour) cells. The chimeric antibody can be used in the diagnosis

XX and treatment of this disease

XX Sequence 11 AA;

XX Query Match 100.0%; Score 59; DB 2; Length 11;

Best local similarity 100.0%; Pred. No. 0.011;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11
 |||||
 DB 1 WGGGTTTVSS 11

RESULT 2
 AAR97333
 ID AAR97333 standard; peptide; 11 AA.
 XX
 AC AAR97333;
 XX
 DT 15-OCT-1996 (first entry)
 XX
 DE Humanised monoclonal antibody heavy chain framework region.
 XX
 KM Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
 KM complementary determining region; anti-carcinoma/lymphoma antigen; CEA;
 KM diagnosis; imaging; therapy; immune response.
 XX
 OS Homo sapiens.
 XX
 PN WO9611013-A1.
 XX
 PD 18-APR-1996.
 XX
 PF 28-SEP-1995; 95WO-US011964.
 XX
 PR 05-OCT-1994; 94US-00318157.
 XX
 PA (IMMU-) IMMUNOMEDICS INC.
 XX
 PI Hansen HJ, Armour KL;
 XX
 DR WPI; 1996-209653/21.
 XX
 PT New humanised anti-CEA monoclonal antibody - having engrafted murine
 PT CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
 XX
 PS Claim 7; Page 40; 62pp; English.
 XX

CC New humanised monoclonal antibodies (MAbs) comprising the complementary
 CC determining regions (CDRs) of a parental murine class III anti-
 CC carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
 CC heterologous antibody which can be derived from any species including
 CC human, retain the anti-CEA binding specificity of the parental murine MAb
 CC but are less immunogenic in a human subject than the parental MAb. The
 CC humanised antibodies can be used in diagnosis, imaging and therapy of CEA
 CC -producing cancers and patients receiving the humanised antibodies and
 CC conjugates show improved therapeutic results, decreased immune responses
 CC and decreased immune-mediated adverse effects compared to the parent
 CC antibody. This sequence corresponds to the fourth framework region of the
 CC heavy chain of the humanised MAb. See AAR97333-97333
 CC
 XX

Sequence 11 AA;

Query Match 100.0%; Score 59; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11
 |||||
 DB 1 WGGGTTTVSS 11

RESULT 3
 AAU07452
 ID AAU07452 standard; peptide; 11 AA.
 XX
 AC AAU07452;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DS Synthetic peptide H-FR4-F8.

XX H-FR4-F8; antimicrobial; antiviral; cytostatic; immunomodulatory;
 KM antibody; gene therapy; HIV; human immunodeficiency virus; tumour;
 KM metabolic disorder; immune disorder; auto-immune disorder.
 XX

OS Synthetic.
 XX

PN WO200149713-A2.
 XX

PD 12-JUL-2001.
 XX

PF 29-DEC-2000; 2000WO-IT000554.
 XX

PR 30-DEC-1999; 99IT-RM000803.
 XX

PA (CNEN) ENEA ENTERNOVE TECNOLOGIE ENERGIA.
 PA (CONS-) SOC CONSORTILE METAPONTUM AGROBIOS SRL.
 XX

PI Benvenuto E, Franconi R, Desiderio A, Tavadoraki P;
 XX

DR WPI; 2001-502555/55.
 DR N-P8DB; AAS11874.
 XX

PT Peptides which are able to confer stability and solubility to an antibody
 PT comprising these peptides, useful for treating pathologies (e.g. tumor)
 PT associated with accumulation of a molecule inside or outside a human, or
 PT animal cell.
 XX

Claim 1; Page 57; 109pp; English.
 XX

CC The invention relates to peptides which are able to confer stability and
 CC solubility to an antibody comprising these peptides. The peptides are
 CC especially H-FR1, H-FR2, HP-R3, HPR4, L-FR1, L-FR2, L-FR3 or L-FR4
 CC present within a variable region of an antibody which makes the antibody
 CC soluble and stable in cytoplasm. Peptides having the sequences of HFR1 to
 CC H-FR4 are present within the variable region of the heavy chain of an
 CC antibody, covalently linked to the H-CDR1, H-CDR2, H-CDR3 in the order (H
 CC -FR1)-(H-CDR1)-(H-FR2)-(H-CDR2)-(H-FR3)-(H-CDR3)-(H-CDR4) and peptides
 CC having the sequences of L-FR1 to L-FR4 are present within the variable
 CC region of the light chain of an antibody, covalently linked to the L-
 CC CDR1, L-CDR2, L-CDR3 in the order (L-FR1)-(L-CDR1)-(L-FR2)-(L-CDR2)-(L-
 CC L-FR3)-(L-CDR3)-(L-CDR4). The antibodies and polynucleotides are useful
 CC (e.g. by gene therapy) for the manufacture of a medicament for the
 CC treatment of pathologies associated with accumulation of a molecule
 CC inside or outside a human, animal cell or plant cell. The pathologies are
 CC infectious (e.g. viral infections such as HIV, human immunodeficiency
 CC virus, infections), tumour, metabolic and immune (especially auto-immune)
 CC pathologies. The present sequence represents the peptide H-FR4-F8 (also
 CC known as H-FR4)
 CC
 XX

Sequence 11 AA;

Query Match 100.0%; Score 59; DB 4; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11
 |||||
 DB 1 WGGGTTTVSS 11

RESULT 4
 AAE28561
 ID AAE28561 standard; peptide; 11 AA.
 XX
 AC AAE28561;
 XX
 DT 27-DEC-2002 (first entry)
 XX
 DE scFv antibody heavy chain framework region 4 from S18 clone.
 XX
 KM Human; sugar-nucleic acid interaction; single chain human antibody; scFv;
 KM L-peptide binder; D-nucleic acid binder; sugar-protein interaction; FR4;

PA (EPIC-) EPICYTE PHARM INC.

DR WPI; 2002-055482/07.

PT Preparing immunoglobulin binding protein array in plant cells by transforming the cells with different polynucleotides encoding binding

PT protein polypeptides specific to ligand, selecting plant cells for
PT preparing array.

PS Disclosure; Fig 1B; 129pp; English.

XX
XX
XX The invention relates to transforming a population of cells (e.g. plant
cells), comprising using a library of two different polynucleotides
CC encoding different immunoglobulin binding protein (IgBP) polypeptides
CC that specifically bind to a ligand or form one or more disulphide bonds
CC with polypeptides in transfected cells, to generate an IgBP that binds to
CC a ligand, and transformed plant cells are selected, and preparing an IgBP
CC array in plant cells. At least one peptide sequence has at least 75%
CC sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
CC IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
CC useful for preparing an immunoglobulin binding protein array, preferably
CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
CC discovery of e.g. screening assays of IgBPs having desired
CC characteristics. The present invention is a mammalian immunoglobulin
CC derived peptide that may be incorporated into an IgBP of the invention

XX Sequence 11 AA;

Query Match 100.0%; Score 59; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTWSS 11
| | | | | | | | | | | |
DB 1 WGGGTTVTWSS 11

RESULT 9

ABO10719 standard; peptide; 11 AA.

AC ABO10719;

DT 20-AUG-2003 (first entry)

XX Deimmunised murine J415-4 antibody framework sequence VHFR4.

XX Modified antibody; deimmunised antibody; anti-PSMA antibody;

XX prostate specific membrane antigen; immunogenic; CDR; murine;

XX complementary determining region; J591; J415; J533; B99; mouse;

XX prostatic disorder; cancerous disorder; genitourinary inflammation;

XX prostatitis; benign enlargement; prostatic cancer; testicular cancer;

XX solid tumour; soft tissue tumour; metastatic lesion; pain; analgesic;

XX antiinflammatory; cytostatic; framework region; variable heavy chain;

XX variable light chain; VH; VL; variable region; mutant; mutein.

OS Mus musculus.

XX Synthetic.

XX WO200298897-A2.

XX 12-DEC-2002.

XX 30-MAY-2002; 2002WO-US017068.

XX 01-JUN-2001; 2001US-0295214P.

XX 20-SEP-2001; 2001US-0323585P.

XX 08-MAR-2002; 2002US-0362810P.

XX (CORR) CORNELL RES FOUND INC.

XX Bander N, Carr FJ, Hamilton A;

XX WPI; 2003-156839/15.

XX New modified anti-prostate specific membrane antigen (PSMA)

PT immunoglobulins, useful for treating or preventing a prostatic or

PT cancerous disorder, e.g. genitourinary inflammation, prostatitis, or
PT prostatic or testicular cancer.

PS Disclosure; Page 21; 254pp; English.

XX
XX
XX The present invention relates to modified (e.g. deimmunised) antibodies
CC to prostate specific membrane antigen (PSMA). The modified anti-PSMA
CC antibodies are less immunogenic compared to the unmodified anti-PSMA
CC antibodies. The modified antibodies comprise complementarity determining
CC regions (CDRs) from a non-human antibody (e.g. murine antibody J591, J415,
CC J533 or B99), and framework sequences that are less immunogenic in humans
CC (e.g. less antigenic than the murine frameworks in which a murine CDR
CC naturally occurs). The modified antibodies bind with PSMA, preferably
CC human PSMA, with high affinity and specificity. The anti-PSMA antibodies
CC are useful for treating or preventing a prostatic or cancerous disorder,
CC e.g. genitourinary inflammation, prostatitis, benign enlargement,
CC prostatic cancer or testicular cancer, or solid tumours, soft tissue
CC tumours or metastatic lesions, and its associated pain. The present
CC sequence represents a deimmunised murine framework region

XX Sequence 11 AA;

Query Match 100.0%; Score 59; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTWSS 11
| | | | | | | | | | | |
DB 1 WGGGTTVTWSS 11

RESULT 10

ABR44663 standard; peptide; 11 AA.

AC ABR44663;

DT 25-JUL-2003 (first entry)

XX Murine J415-4 antibody VH FR4 amino acid sequence SEQ ID NO:40.

XX Mouse; murine; antibody; skin disorder; binding agent; PSMA; cytostatic;

XX prostate specific membrane antigen; antipsoriatic; antiarthritic;

XX dermatological; antiinflammatory; antiallergic; vaccine; dermal disorder;

XX epidermal disorder; psoriasis; inflammatory disorder; epidermis; dermis;

XX neoplastic disorder.

XX Mus musculus.

XX Synthetic.

XX WO2003024388-A2.

XX 27-MAR-2003.

XX 30-MAY-2002; 2002WO-US017204.

XX 20-SEP-2001; 2001US-0324100P.

XX 08-MAR-2002; 2002US-0362612P.

XX (CORR) CORNELL RES FOUND INC.

XX Bander N;

XX WPI; 2003-313319/30.

XX Ablating/killing aberrant prostate specific membrane antigen-expressing

PT cells for treating skin disorders, by contacting the cell with an

PT antibody that binds to the extracellular domain of prostate specific

PT membrane antigen.

PS Disclosure; Page 68; 225pp; English.

XX The present invention describes a method (M1) for ablating or killing an

CC excessive T cell or neutrophil activity. Accordingly, these IL-9
CC antagonists exhibit antiallergic, antiasthmatic and cytoprotective
CC activities. This peptide sequence is a peptide from the human heavy chain
CC framework region 4, used in an exemplification of the invention.

XX Sequence 11 AA;

Query Match 100.0%; Score 59; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVVSS 11
|||
DB 1 WGGGTTTVVSS 11

RESULT 13

ADH17960
ID ADH17960 standard; peptide; 11 AA.

XX ADH17960;

DT 11-MAR-2004 (first entry)

XX Human modified 15H12/19D12 HCA framework region 4 peptide.

XX insulin-like growth factor receptor 1; IGFRI; cytoskeletal; osteopathic;
XX antidiabetic; antiproliferative; vasotropic; antidiabetic;
XX acromegaly; bladder cancer; Wilm's tumour; ovarian; pancreatic;
XX benign prostatic hyperplasia; breast; prostate; bone; lung; colorectal;
XX cervical; synovial sarcoma; diarrhoea; carcinoma syndrome;
XX vasodilative intestinal peptide; gigantism; poriasis; atherosclerosis;
XX smooth muscle restenosis; blood vessel; microvascular proliferation;
XX gene therapy; human; 15H12/19D12; heavy chain A; HCA; framework region.

XX Synthetic.

OS Homo sapiens.

XX WO2003100008-A2.

XX 04-DEC-2003.

XX 22-MAY-2003; 2003WO-US016283.

XX 24-MAY-2002; 2002US-0383459P.

XX 02-JUL-2002; 2002US-0393214P.

XX 23-DEC-2002; 2002US-0436254P.

XX (SCHE) SCHERING CORP.

XX Wang Y, Greenberg R, Presta L, Pachter JA, Hailey J, Brame P;

XX Williams D, Srinivasan M, Feingersh D;

XX WPI: 2004-042807/04.

XX N-PDB; ADH17959.

XX New binding composition that specifically binds to insulin-like growth
XX factor receptor 1, useful for treating or preventing a medical condition
XX that is mediated by elevated expression or activity of IGFRI.

XX Disclosure; SEQ ID NO 69; 144pp; English.

XX The invention relates to a novel binding composition that specifically
XX binds to insulin-like growth factor receptor 1 (IGFRI). The composition
XX of the invention demonstrates cytoskeletal, osteopathic,
XX antidiabetic, antiproliferative, vasotropic and antidiabetic
XX activities and may be useful for preventing or treating a medical
XX condition selected from acromegaly, bladder cancer, Wilm's cancer,
XX ovarian cancer, pancreatic cancer, benign prostatic hyperplasia, breast
XX cancer, prostate cancer, bone cancer, lung cancer, colorectal cancer,
XX cervical cancer, synovial sarcoma, diarrhoea associated with carcinoma
XX syndrome, vasodilative intestinal peptide secreting tumours, gigantism,
XX poriasis, atherosclerosis, smooth muscle restenosis of blood vessels and

CC inappropriate microvascular proliferation. The composition may also have
CC gene therapy applications. The current sequence is that of the human
CC 15H12/19D12 heavy chain A (HCA) framework region peptide of the
CC invention.

XX Sequence 11 AA;

Query Match 100.0%; Score 59; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVVSS 11
|||
DB 1 WGGGTTTVVSS 11

RESULT 14

ADH18011
ID ADH18011 standard; peptide; 11 AA.

XX ADH18011;

DT 11-MAR-2004 (first entry)

XX Human modified 15H12/19D12 HCB framework region 4 peptide.

XX insulin-like growth factor receptor 1; IGFRI; cytoskeletal; osteopathic;
XX antidiabetic; antiproliferative; vasotropic; antidiabetic;
XX acromegaly; bladder cancer; Wilm's tumour; ovarian; pancreatic;
XX benign prostatic hyperplasia; breast; prostate; bone; lung; colorectal;
XX cervical; synovial sarcoma; diarrhoea; carcinoma syndrome;
XX vasodilative intestinal peptide; gigantism; poriasis; atherosclerosis;
XX smooth muscle restenosis; blood vessel; microvascular proliferation;
XX gene therapy; human; 15H12/19D12; heavy chain B; HCB; framework region.

XX Synthetic.

OS Homo sapiens.

XX WO2003100008-A2.

XX 04-DEC-2003.

XX 22-MAY-2003; 2003WO-US016283.

XX 24-MAY-2002; 2002US-0383459P.

XX 02-JUL-2002; 2002US-0393214P.

XX 23-DEC-2002; 2002US-0436254P.

XX (SCHE) SCHERING CORP.

XX Wang Y, Greenberg R, Presta L, Pachter JA, Hailey J, Brame P;

XX Williams D, Srinivasan M, Feingersh D;

XX WPI: 2004-042807/04.

XX N-PDB; ADH18010.

XX New binding composition that specifically binds to insulin-like growth
XX factor receptor 1, useful for treating or preventing a medical condition
XX that is mediated by elevated expression or activity of IGFRI.

XX Disclosure; SEQ ID NO 120; 144pp; English.

XX The invention relates to a novel binding composition that specifically
XX binds to insulin-like growth factor receptor 1 (IGFRI). The composition
XX of the invention demonstrates cytoskeletal, osteopathic,
XX antidiabetic, antiproliferative, vasotropic and antidiabetic
XX activities and may be useful for preventing or treating a medical
XX condition selected from acromegaly, bladder cancer, Wilm's cancer,
XX ovarian cancer, pancreatic cancer, benign prostatic hyperplasia, breast
XX cancer, prostate cancer, bone cancer, lung cancer, colorectal cancer,
XX cervical cancer, synovial sarcoma, diarrhoea associated with carcinoma
XX syndrome, vasodilative intestinal peptide secreting tumours, gigantism,
XX poriasis, atherosclerosis, smooth muscle restenosis of blood vessels and

CC inappropriate microvascular proliferation. The composition may also have
CC gene therapy applications. The current sequence is that of the human
CC 15H12/19D12 heavy chain B (HCB) framework region peptide of the
CC invention.
XX

Sequence 11 AA;

Query Match 100.0%; Score 59; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. NO. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVYSS 11
|||
Db 1 WGGGTTTVYSS 11

RESULT 15

ADQ90791
ID ADQ90791 standard; protein; 11 AA.

AC ADQ90791;

DT 07-OCT-2004 (first entry)

DE Artificially deimmunised framework sequence #14.

insulin-related disorder; prostate specific membrane antigen; PSMA;
obesity; hyperglycaemia; hypoglycaemia; hyperinsulinaemia;
insulin-resistance; impaired glucose tolerance; impaired fasting glucose;
Type 1 diabetes mellitus; Type 2 diabetes mellitus; gestational diabetes.
Synthetic.

US2004136998-A1.

15-JUL-2004.

17-OCT-2003; 2003US-00688015.

30-OCT-2002; 2002US-0422396P.

(BAND/) BANDER N H.

Bander NH;

WPI; 2004-533338/51.

Use of anti-prostate specific membrane antigen antibodies for treating or
preventing insulin-related disorders, e.g. obesity, hyperglycemia,
hypoglycemia, hyperinsulinemia, insulin-resistance, or Type 1 or 2
diabetes mellitus.

Disclosure; SEQ ID NO 40; 89pp; English.

The invention relates to a method of treating or preventing an insulin-
related disorder in a subject which comprises administering an antibody
or its antigen-binding portion specific for prostate specific membrane
antigen (PSMA). The method is useful for treating an insulin-related
disorder, including obesity, hyperglycaemia, hypoglycaemia,
hyperinsulinaemia, insulin-resistance, impaired glucose tolerance,
impaired fasting glucose, Type 1 diabetes mellitus, Type 2 diabetes
mellitus, and gestational diabetes. The present sequence represents an
artificially deimmunised framework sequence.

Sequence 11 AA;

Query Match 100.0%; Score 59; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. NO. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVYSS 11
|||
Db 1 WGGGTTTVYSS 11

Search completed: December 4, 2005, 04:45:01
Job time : 97.5625 secs

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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:45 ; Search time 15.5833 Seconds

(without alignments)
67.918 Million cell updates/sec

Title: US-10-632-706-198

Perfect score: 59

Sequence: 1 WGGGTTTVSS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 80:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	74	2 S26793	Ig heavy chain V r
2	59	100.0	110	2 PH1655	Ig heavy chain V r
3	59	100.0	113	2 S55533	Ig heavy chain V r
4	59	100.0	113	2 S55535	Ig heavy chain V r
5	59	100.0	113	2 S55530	Ig heavy chain V r
6	59	100.0	113	2 S55534	Ig heavy chain V r
7	59	100.0	113	2 S55528	Ig heavy chain V r
8	59	100.0	113	2 S55532	Ig heavy chain V r
9	59	100.0	113	2 S55531	Ig heavy chain V r
10	59	100.0	114	2 S46392	Ig heavy chain V r
11	59	100.0	114	2 S20707	Ig heavy chain V r
12	59	100.0	115	2 S20706	Ig heavy chain V r
13	59	100.0	116	2 S15672	Ig heavy chain V r
14	59	100.0	116	2 S55542	Ig heavy chain V r
15	59	100.0	117	2 S55541	Ig heavy chain V r
16	59	100.0	118	2 PH1666	Ig heavy chain V r
17	59	100.0	118	2 PH1660	Ig heavy chain V r
18	59	100.0	118	2 S32786	Ig heavy chain V r
19	59	100.0	119	2 PH0961	Ig heavy chain (an
20	59	100.0	120	2 PH1650	Ig heavy chain V r
21	59	100.0	120	2 S49590	Ig heavy chain V r
22	59	100.0	120	2 PD0008	Ig heavy chain V r
23	59	100.0	120	2 S55538	Ig heavy chain V r
24	59	100.0	120	2 S55539	Ig heavy chain V r
25	59	100.0	120	2 S55537	Ig heavy chain V r
26	59	100.0	120	2 S55536	Ig heavy chain V r
27	59	100.0	120	2 S12953	Ig heavy chain V r
28	59	100.0	121	2 S31106	Ig heavy chain - h
29	59	100.0	121	2 S55540	Ig heavy chain V r

30	59	100.0	122	2 E36005	Ig heavy chain V r
31	59	100.0	122	2 PH0958	Ig heavy chain V r
32	59	100.0	123	2 S26794	Ig heavy chain V r
33	59	100.0	124	2 S20775	Ig heavy chain V r
34	59	100.0	125	2 S37455	Ig mu chain - huma
35	59	100.0	125	2 S24686	Ig heavy chain V6
36	59	100.0	127	2 S56213	Ig heavy chain V r
37	59	100.0	127	2 S24689	Ig heavy chain V6
38	59	100.0	128	2 S48797	Ig heavy chain V r
39	59	100.0	131	2 S66537	Ig heavy chain V r
40	59	100.0	132	2 PH0954	Ig heavy chain V r
41	59	100.0	133	2 C33548	Ig heavy chain V-1
42	59	100.0	135	2 B32274	Ig heavy chain pre
43	59	100.0	135	2 S78051	Ig heavy chain pre
44	59	100.0	136	2 PH0960	Ig heavy chain V r
45	59	100.0	137	2 S31676	Ig heavy chain V r

ALIGNMENTS

RESULT 1
S26793
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26793
R:Morfari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A:Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fam
A:Reference number: S26786; MUID:92111632; PMID:1730251
A:Accession: S26793
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-74 <MOR>
A:Cross-references: UNIPARC:UPI000115FCA; EMBL:X61019; NID:932787; PIDN:CAA43353.1; PID
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 100.0%; Score 59; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
|||||
Db 64 WGGGTTTVSS 74

RESULT 2

PH1655
Ig heavy chain V region (clone 2E8) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C:Accession: PH1655
R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Saseo, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyloc
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1655
A:Molecule type: mRNA
A:Residues: 1-110 <HIL>
A:Cross-references: UNIPARC:UPI0000176BDC
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMW>

Query Match 100.0%; Score 59; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
|||||

Db 100 WGGTTTVSS 110

RESULT 3

SS5533
Ig heavy chain V region pe25 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
C:Accession: S55533
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using
A:Reference number: S55528; MUID:95239763; PMID:7536850
A:Accession: S55533
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <BOB>
A:Cross-references: UNIPARC:UPI0000116205; EMBL:X82594; NID:9854314; PIDN:CAA57930.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGTTTVSS 11
|||||
Db 103 WGGTTTVSS 113

RESULT 4

SS5535
Ig heavy chain V region pe23 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
C:Accession: S55535
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using
A:Reference number: S55528; MUID:95239763; PMID:7536850
A:Accession: S55535
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <BOB>
A:Cross-references: UNIPARC:UPI0000116203; EMBL:X82592; NID:9854310; PIDN:CAA57928.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGTTTVSS 11
|||||
Db 103 WGGTTTVSS 113

RESULT 5

SS5530
Ig heavy chain V region pe17 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
C:Accession: S55530
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using
A:Reference number: S55528; MUID:95239763; PMID:7536850
A:Accession: S55530

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <BOB>
A:Cross-references: UNIPARC:UPI00001161FB; EMBL:X82586; NID:9854296; PIDN:CAA57922.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGTTTVSS 11
|||||
Db 103 WGGTTTVSS 113

RESULT 6

SS5534
Ig heavy chain V region pe15 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
C:Accession: S55534
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using
A:Reference number: S55528; MUID:95239763; PMID:7536850
A:Accession: S55534
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <BOB>
A:Cross-references: UNIPARC:UPI00001161FC; EMBL:X82584; NID:9854292; PIDN:CAA57920.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGTTTVSS 11
|||||
Db 103 WGGTTTVSS 113

RESULT 7

SS5528
Ig heavy chain V region (pe16/pe14) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
C:Accession: S55528; S55529
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using
A:Reference number: S55528; MUID:95239763; PMID:7536850
A:Accession: S55528
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <BOB>
A:Cross-references: UNIPARC:UPI00001161FB; EMBL:X82585; NID:9854294; PIDN:CAA57921.1; PI
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.0033;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTYSS 11
|||||

Db 103 WGGGTTVTYSS 113

RESULT 8

S55532

Ig heavy chain V region pe19 - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000

C/Accession: S55532

R/Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using

A/Reference number: S55528; MUID:95239763; PMID:7536850

A/Accession: S55532

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-113 <BOE>

A/Cross-references: UNIPARC:UPI00001161PF; EMBL:X82588; NID:9854300; PIDN:CAA57924.1; PI

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/12-97/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 59; DB 2; Length 113;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTYSS 11
|||||

Db 103 WGGGTTVTYSS 113

RESULT 9

S55531

Ig heavy chain V region pe18 - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000

C/Accession: S55531

R/Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using

A/Reference number: S55528; MUID:95239763; PMID:7536850

A/Accession: S55531

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-113 <BOE>

A/Cross-references: UNIPARC:UPI00001161FE; EMBL:X82587; NID:9854298; PIDN:CAA57923.1; PI

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/12-97/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 59; DB 2; Length 113;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTYSS 11
|||||

Db 103 WGGGTTVTYSS 113

RESULT 10

S46392

Ig heavy chain V region (VH-28) - human

C/Species: Homo sapiens (man)

C/Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000

C/Accession: S46392

R/Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.

J. Mol. Biol. 239, 66-78, 1994

A/Title: In vitro assembly of repertoires of antibody chains on the surface of phage by

A/Reference number: S46390; MUID:94254092; PMID:8196048

A/Accession: S46392

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-114 <FIG>

A/Cross-references: UNIPARC:UPI00001137D6; EMBL:Z31688; NID:9499306; PIDN:CAA83493.1; PI

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/15-98/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 59; DB 2; Length 114;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTYSS 11
|||||

Db 104 WGGGTTVTYSS 114

RESULT 11

S20707

Ig heavy chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000

C/Accession: S20707

R/Brennan, D.M.; Hinds, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.; Oeb

submitted to the EMBL Data Library, April 1992

A/Description: Binding specificity and variable region sequences of two monoclonal anti

A/Reference number: S20706

A/Accession: S20707

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-114 <BRE>

A/Cross-references: UNIPARC:UPI0000176B37; EMBL:Z11916

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/12-95/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 59; DB 2; Length 114;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTYSS 11
|||||

Db 104 WGGGTTVTYSS 114

RESULT 12

S20706

Ig heavy chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C/Accession: S20706

R/Brennan, D.M.; Hinds, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.; Oeb

submitted to the EMBL Data Library, April 1992

A/Description: Binding specificity and variable region sequences of two monoclonal anti

A/Reference number: S20706

A/Accession: S20706

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-115 <BRE>

A/Cross-references: UNIPARC:Q8R3V9; UNIPARC:UPI0000176C45; EMBL:Z11914

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F/12-97/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 100.0%; Score 59; DB 2; Length 115;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTYSS 11
|||||

Db 105 WCGGTTVTSS 115

RESULT 13

IG heavy chain V region - mouse (fragment)
S15672
C:Species: Mus musculus (house mouse)
C:Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S15672
R:Tempest, P.R.; Bremner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harris, B.; Technology 9, 266-271, 1991
A:Title: Reshaping a human monoclonal antibody to inhibit human respiratory syncytial virus
A:Reference number: S15672; MUID:91337412; PMID:1367535
A:Accession: S15672
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-116 <TRM>
A:Cross-references: UNIPARC:UPI0000115F4C; EMBL:X58835; NID:951978; PIDN:CAA41644.1; PIDN:CAA41644.1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGGTTVTSS 11
|||||
Db 106 WCGGTTVTSS 116

RESULT 14

S55542
IG heavy chain V region pe2 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C:Accession: S55542
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using
variations in the variable region genes.
A:Reference number: S55528; MUID:95239763; PMID:7536850
A:Accession: S55542
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-116 <BOE>
A:Cross-references: UNIPARC:UPI00001161F9; EMBL:X82581; NID:9854302; PIDN:CAA57917.1; PIDN:CAA57917.1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGGTTVTSS 11
|||||
Db 106 WCGGTTVTSS 116

RESULT 15

S55541
IG heavy chain V region pa1 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C:Accession: S55541
R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.
J. Mol. Biol. 247, 932-946, 1995
A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using
variations in the variable region genes.
A:Reference number: S55528; MUID:95239763; PMID:7536850
A:Accession: S55541
A:Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-117 <BOE>
A:Cross-references: UNIPARC:UPI00001161F8; EMBL:X82580; NID:9854286; PIDN:CAA57916.1; PIDN:CAA57916.1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 59; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGGTTVTSS 11
|||||
Db 107 WCGGTTVTSS 117

Search completed: December 4, 2005, 04:53:46
Job time : 15.5833 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:31:36 ; Search time 100.375 Seconds
(without alignment)
77.318 Million cell updates/sec

Title: US-10-632-706-198

Perfect score: 59

Sequence: 1 MGCGTTTVSS 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : uniprot_05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	119	2 Q9GYZ2_MOUSE	Q9GYZ2 mus musc
2	59	100.0	121	2 Q8CGS2_MOUSE	Q8CGS2 mus musc
3	59	100.0	146	1 HV21_HUMAN	P06331 homo sapien
4	59	100.0	147	1 HV1C_HUMAN	P01744 homo sapien
5	59	100.0	147	2 Q925S3_MOUSE	Q925S3 mus musc
6	59	100.0	159	2 Q96G80_HUMAN	Q96G80 homo sapien
7	59	100.0	170	2 Q925S2_MOUSE	Q925S2 mus musc
8	59	100.0	218	2 Q925S1_MOUSE	Q925S1 mus musc
9	59	100.0	241	2 Q921A6_MOUSE	Q921A6 mus musc
10	59	100.0	348	2 Q6PYX1_HUMAN	Q6PYX1 homo sapien
11	59	100.0	416	2 Q9NP65_HUMAN	Q9NP65 homo sapien
12	59	100.0	472	2 Q6N089_HUMAN	Q6N089 homo sapien
13	59	100.0	573	2 Q8WU38_HUMAN	Q8WU38 homo sapien
14	59	100.0	576	2 Q6P418_HUMAN	Q6P418 homo sapien
15	59	100.0	595	2 Q8WUX4_HUMAN	Q8WUX4 homo sapien
16	59	100.0	597	2 Q9BU10_HUMAN	Q9BU10 homo sapien
17	59	100.0	597	2 Q9BOB8_HUMAN	Q9BOB8 homo sapien
18	59	100.0	597	2 Q6GKX5_HUMAN	Q6GKX5 homo sapien
19	59	100.0	606	2 Q6GMY2_HUMAN	Q6GMY2 homo sapien
20	59	100.0	625	2 Q6PAA6_HUMAN	Q6PAA6 homo sapien
21	59	98.3	465	2 Q6PJB2_MOUSE	Q6PJB2 mus musc
22	58	98.3	468	2 Q569W9_MOUSE	Q569W9 mus musc
23	58	98.3	468	2 Q505N9_MOUSE	Q505N9 mus musc
24	58	98.3	471	2 Q6K04_MOUSE	Q6K04 mus musc
25	58	98.3	472	2 Q6PJA7_MOUSE	Q6PJA7 mus musc
26	58	98.3	473	2 Q91205_MOUSE	Q91205 mus musc
27	58	98.3	476	2 Q569X1_MOUSE	Q569X1 mus musc
28	58	98.3	477	2 Q58B56_MOUSE	Q58B56 mus musc
29	58	98.3	486	2 Q91207_MOUSE	Q91207 mus musc
30	58	98.3	487	2 Q99KA4_MOUSE	Q99KA4 mus musc
31	56	94.9	109	2 Q9JL75_MOUSE	Q9JL75 mus musc

32	56	94.9	111	1 HV35_MOUSE	P01804 mus musc
33	56	94.9	114	2 Q9JL81_MOUSE	Q9JL81 mus musc
34	56	94.9	117	2 Q9QXFO_MOUSE	Q9QXFO mus musc
35	56	94.9	118	1 HV39_MOUSE	P01809 mus musc
36	56	94.9	118	2 Q921C4_MOUSE	Q921C4 mus musc
37	56	94.9	120	1 HV03_MOUSE	P01747 mus musc
38	56	94.9	121	1 HV01_MOUSE	P01745 mus musc
39	56	94.9	134	2 Q65ZF6_MOUSE	Q65ZF6 mus musc
40	56	94.9	136	1 HV15_MOUSE	P01759 mus musc
41	56	94.9	137	1 HV11_MOUSE	P01755 mus musc
42	56	94.9	137	1 HV46_MOUSE	P01822 mus musc
43	56	94.9	137	2 Q924R6_MOUSE	Q924R6 mus musc
44	56	94.9	139	1 HV07_MOUSE	P01751 mus musc
45	56	94.9	140	2 Q924P8_MOUSE	Q924P8 mus musc

ALIGNMENTS

```

RESULT 1
Q9GYZ2_MOUSE
AC Q9GYZ2_MOUSE PRELIMINARY; PRT; 119 AA.
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2003 (TREMBLrel. 25, Last sequence update)
DE Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30 heavy
DE chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Song X.T., Feng Z.Q., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282622; AAG01452.1; -, mRNA.
DR HSSP; P01751; 1A6W.
DR SMR; Q9GYZ2; 1-119.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IG_V.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13567 MW; BA893873FDP5FA6AB CRC64;

Query Match 100.0%; Score 59; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGCGTTTVSS 11
Db 109 MGCGTTTVSS 119

RESULT 2
Q8CGS2_MOUSE
ID Q8CGS2_MOUSE PRELIMINARY; PRT; 121 AA.
AC Q8CGS2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Anti-deoxyribovalenol scfv lambda heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.

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OK NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-BALB/c;
RA Wang Z., Munshi K., Osawa F., Pescka J.J., Hart L.P.,
RL Submitted (Sep-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY151140; AAN75452.1; -, mRNA.
DR HSSP; P01751; INGB.
DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV, 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 121
FT SEQUENCE 121 AA; 13475 MW; 84FE6CFA8053F5D6 CRC64;
SQ
Query Match 100.0%; Score 59; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WGGGTTVTSS 11
DB 111 WGGGTTVTSS 121
RESULT 3
HY21_HUMAN STANDARD; PRT; 146 AA.
AC P06331;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DS Ig heavy chain V-II region ARH-77 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=85205332; PubMed=3922855; DOI=10.1016/0378-1119(85)90092-7;
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
RT repeat sequence in 5' flanking region.";
RL Gene 33:181-189(1985).
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
CC
CC PIR; A02101; G1H0H2.
DR HSSP; P01825; 7FAB.
DR SMR; P06331; 21-146.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV, 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 146 Ig heavy chain V-II region ARH-77.
FT REGION 20 117 V segment.
FT REGION 118 127 D segment.
FT REGION 128 146 J segment.
FT DISULFID 42 115 By similarity.
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52B8218171F CRC64;

Query Match 100.0%; Score 59; DB 1; Length 146;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WGGGTTVTSS 11
DB 136 WGGGTTVTSS 146
RESULT 4
HY1C_HUMAN STANDARD; PRT; 147 AA.
ID HY1C_HUMAN STANDARD; PRT; 147 AA.
AC P01744;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DS Ig heavy chain V-I region ND precursor (fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [2]
RP PROTEIN SEQUENCE OF 20-147.
RA Benich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (in) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC -1- MISCELLANEOUS: This epsilon chain was isolated from a myeloma
CC protein.
CC
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC HSSP; P01751; INGB.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV, 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Pyrolydione carboxylic acid; Signal.
FT SIGNAL 1 19
FT CHAIN 20 147 Ig heavy chain V-I region ND.
FT DOMAIN 20 131 Ig-like.
FT MOD_RES 20 20 Pyrolydione carboxylic acid.
FT DISULFID 41 115
FT CONFLICT 21 21 T -> V (in Ref. 2).
FT CONFLICT 53 54 IH -> HI (in Ref. 2).
FT CONFLICT 67 68 VG -> GV (in Ref. 2).
FT CONFLICT 125 125 Missing (in Ref. 2).
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 16496 MW; 948F9F72A536C20 CRC64;
Query Match 100.0%; Score 59; DB 1; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.0067;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WGGGTTVTSS 11

Db 137 WGGGTTTVSS 147

RESULT 5

Q925S3_MOUSE PRELIMINARY; PRT; 147 AA.

AC Q925S3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE MRP3
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

NP NUCLEOTIDE SEQUENCE.

RC STRAIN=BALB/c;

RX PubMed=11819679;

RA Cui D.X., Zeng G.Y., Wang F., Xu J.R., Ren D.Q., Guo Y.H., Tian F.R.,
Yan X.J., Hou Y., Su C.Z.;

RT "Mechanism of exogenous nucleic acids and their precursors improving
the repair of intestinal epithelium after gamma-irradiation in mice.";
World J. Gastroenterol. 6:709-717(2000).

RL NUCLEOTIDE SEQUENCE.

RP STRAIN=BALB/c;

RC Cui D., Zeng G., Yan X., Li X., Su C.;

RT "Cloning of mouse genes related to repairing of intestinal epithelium
of the irradiated mice by treatment with the intestinal RNA of mice of
the same strain.";

RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).

DR EMBL: AF240166; AAK43731.1; -; mRNA.

DR HSSP: P01751; 1A6W.

DR SMR: Q925S3; 3-139.

DR InterPro: IPR007110; Ig-like.

DR InterPro: IPR003596; Ig_v.

DR SMART: SM00406; IGV; 1.

DR PROSITE: PS50835; IG_LIKE; 1.

KW Immunoglobulin domain.

SQ SEQUENCE 147 AA; 16274 MW; 800594A12B97191F CRC64;

Query Match 100.0%; Score 59; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 0.0067;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11

Db 111 WGGGTTTVSS 121

RESULT 6

Q96QSO_HUMAN PRELIMINARY; PRT; 159 AA.

AC Q96QSO;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Putative matrix cell adhesion molecule-3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;

OC Homo

NCBI_TaxID=9606;

NP NUCLEOTIDE SEQUENCE.

RP TILSON M.D.;

RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY339025; AAK62649.1; -; mRNA.

DR HSSP: P01869; 1A66.

DR InterPro: IPR007110; Ig-like.

DR InterPro: IPR003596; Ig_v.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 159 AA; 17497 MW; 5D29537E881FAF02 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11

Db 139 WGGGTTTVSS 149

RESULT 7

Q925S2_MOUSE PRELIMINARY; PRT; 170 AA.

AC Q925S2;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE MRP4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidae; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

NP NUCLEOTIDE SEQUENCE.

RC STRAIN=BALB/c;

RX PubMed=11819679;

RA Cui D.X., Zeng G.Y., Wang F., Xu J.R., Ren D.Q., Guo Y.H., Tian F.R.,
Yan X.J., Hou Y., Su C.Z.;

RT "Mechanism of exogenous nucleic acids and their precursors improving
the repair of intestinal epithelium after gamma-irradiation in mice.";
World J. Gastroenterol. 6:709-717(2000).

RL NUCLEOTIDE SEQUENCE.

RP STRAIN=BALB/c;

RC Cui D., Zeng G., Yan X., Li X., Su C.;

RT "Cloning of mouse genes related to repairing of intestinal epithelium
of the irradiated mice by treatment with the intestinal RNA of mice of
the same strain.";

RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).

DR EMBL: AF240167; AAK43732.1; -; mRNA.

DR HSSP: P01751; 1A6W.

DR SMR: Q925S2; 3-124.

DR InterPro: IPR007110; Ig-like.

DR InterPro: IPR003596; Ig_v.

DR SMART: SM00406; IGV; 1.

DR PROSITE: PS50835; IG_LIKE; 1.

KW Immunoglobulin domain.

SQ SEQUENCE 170 AA; 17978 MW; 5042823C6C10F38 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11

Db 113 WGGGTTTVSS 123

RESULT 8

Q925S1_MOUSE PRELIMINARY; PRT; 218 AA.

AC Q925S1;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE MRP5 (Fragment).

OS Mus musculus (Mouse).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OK NCBI_TaxId=10090;
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D.X., Zeng G.Y., Wang F., Xu J.R., Ren D.Q., Guo Y.H., Tian P.R.,
RA Yan X.J., Hou Y., Su C.Z.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after gamma-irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR HSP; P01665; 1QNZ.
DR Ensembl; ENSMUSG0000058040; Mus musculus.
DR InterPro; IPR007110; IG_1like.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER
SQ SEQUENCE 218 AA; 23013 MW; 527B4FA8F7982817 CRC64;

Query Match
Best Local Similarity 100.0%; Score 59; DB 2; Length 218;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
DB 110 WGGGTTTVSS 120

RESULT 9
Q921A6_MOUSE
ID Q921A6_MOUSE PRELIMINARY; PRT; 241 AA.
AC Q921A6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-CEA 79 single chain Fv (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OK NCBI_TaxId=10090;
RN
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819(1997).
[2]
RN NUCLEOTIDE SEQUENCE.
RC MEDLINE=9141421; PubMed=1908510; DOI=10.1084/jem.174.3.613;
RA Stark S.E., Caton A.J.;
RT "Antibodies that are specific for a single amino acid interchange in a
RT protein epitope use structurally distinct variable regions.";
RL J. Exp. Med. 174:613-624(1991)
EMBL; U8067; AAB8044.1; -, mRNA.
DR PIR; S1965; S1965.
DR PIR; S1967; S1967.
DR PIR; S1968; S1968.

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DR PIR; S26325; S26325.
DR HSP; P01607; 1BMW.
DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
FT NON_TER
SQ SEQUENCE 241 AA; 26086 MW; 0276887248B9C771 CRC64;

Query Match
Best Local Similarity 100.0%; Score 59; DB 2; Length 241;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
DB 108 WGGGTTTVSS 118

RESULT 10
Q6PYX1_HUMAN
ID Q6PYX1_HUMAN PRELIMINARY; PRT; 348 AA.
AC Q6PYX1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hepatitis B virus receptor binding protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OK NCBI_TaxId=9606;
RN
RP NUCLEOTIDE SEQUENCE.
RA Zhu N.S., Chen Y.Y.;
RL Submitted (MAR-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY570731; AAS88328.1; -, mRNA.
DR PDB; 1T89; X-ray; A/B=..
DR SMR; Q6PYX1; 3-348.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; IG_1like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF07654; C1-rec; 3.
DR SMART; SM00407; IGC1; 3.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Receptor.
FT NON_TER
SQ SEQUENCE 348 AA; 38162 MW; DD96C3D7E0B5E845 CRC64;

Query Match
Best Local Similarity 100.0%; Score 59; DB 2; Length 348;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
DB 8 WGGGTTTVSS 18

RESULT 11
Q9NPP6_HUMAN
ID Q9NPP6_HUMAN PRELIMINARY; PRT; 416 AA.
AC Q9NPP6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Immunoglobulin heavy chain variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.

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OX NCBI_TaxID=9606;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Auffray C., Anorge W., Ballabio A., Estivill X., Gibson K.,
RA Lehrach H., Poustka A., Lundeberg J.
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Pluvinet R., Estivill X., Escarceller M., Sumoy L.
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL389978; CAB97534.1; -; mRNA.
DR HSSP; P01876; 10M0.
DR SMR; Q9NP66; 186-394.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-sect; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
FT NON TER 1
SQ SEQUENCE 416 AA; 44786 MW; 8C41708B8AB4687 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTVTWSS 11
DB 66 WGGGTTVTWSS 76

RESULT 12
O6N089_HUMAN PRELIMINARY; PRT; 472 AA.
ID O6N089_HUMAN
AC O6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686P15220.
GN Name=DKFZp686P15220;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Rectum tumor;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oeanger A.,
RA Fobbo G., Han M., Wiemann S.
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX40627; CAE45781.1; -; mRNA.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-sect; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D046D279 CRC64;

Query Match 100.0%; Score 59; DB 2; Length 472;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 WGGGTTVTWSS 11
DB 132 WGGGTTVTWSS 142

RESULT 13
O8W038_HUMAN PRELIMINARY; PRT; 573 AA.
ID O8W038_HUMAN
AC O8W038;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGH protein.
GN Name=IGH;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hirschhorn S.F., Zeeberg B., Bueltow K.H., Scheefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywicki M.I., Skalska U., Skalska D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN (2)
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-cells;
RA Director MGC Project;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN (3)
RP PROTEIN SEQUENCE.
RX PubMed=1555592;
RA Makiya R., Stigbrand T.
RT "Placental alkaline phosphatase has a binding site for the human
immunoglobulin-G Fc portion."
RL Eur. J. Biochem. 205:341-345 (1992).
DR EMBL; BC021276; AAH21276.1; -; mRNA.
DR PIR; S21205; S21205.
DR PIR; S30532; S30532.
DR HSSP; P18529; 118K.
DR InterPro; ENSG00000196122; Homo sapiens.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-sect; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR Immunoglobulin domain. Repeat.
SQ SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;
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Query Match 100.0%; Score 59; DB 2; Length 595;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGQGTIVTVSS 11
|||
Db 141 MGQGTIVTVSS 151

Search completed: December 4, 2005, 04:52:27
Job time : 102.375 secs

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OM protein - protein search, using sw model

Run on: December 4, 2005, 03:59:51 ; Search time 23.6042 Seconds
(without alignments)
38.528 Million cell updates/sec

Title: US-10-632-706-198

Perfect score: 59

Sequence: 1 WGGTTTVVSS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:*
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3: /cgn2_6/prodata/1/iaa/H.COMB.pep:*
4: /cgn2_6/prodata/1/iaa/PCTUS.COMB.pep:*
5: /cgn2_6/prodata/1/iaa/RE.COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfillsl1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	11	1	US-08-471-780C-120
2	59	100.0	11	1	US-08-467-282B-120
3	59	100.0	11	1	US-08-471-282A-120
4	59	100.0	11	1	US-08-318-157B-40
5	59	100.0	11	1	US-08-468-710C-120
6	59	100.0	11	2	US-08-468-739C-120
7	59	100.0	11	2	US-08-466-265A-114
8	59	100.0	11	2	US-08-466-265A-129
9	59	100.0	11	2	US-09-253-794-40
10	59	100.0	11	2	US-09-563-222C-146
11	59	100.0	11	2	US-09-563-222C-169
12	59	100.0	11	2	US-09-269-921-137
13	59	100.0	11	2	US-09-293-769A-120
14	59	100.0	13	6	5189147-14
15	59	100.0	15	1	US-08-765-179B-8
16	59	100.0	15	6	5189147-20
17	59	100.0	16	4	PCT-US91-02942-91
18	59	100.0	20	2	US-10-194-975-107
19	59	100.0	22	4	PCT-US91-02942-100
20	59	100.0	29	1	US-08-053-131-73
21	59	100.0	29	1	US-08-645-641-73
22	59	100.0	29	1	US-07-853-408B-73
23	59	100.0	29	1	US-08-096-762-73
24	59	100.0	29	1	US-08-308-865-73
25	59	100.0	29	2	US-09-042-353-270
26	59	100.0	29	2	US-08-758-417A-118
27	59	100.0	29	4	PCT-US92-10983-73

28	59	100.0	31	1	US-08-053-131-83	Sequence 83, Appl
29	59	100.0	31	1	US-08-645-641-83	Sequence 83, Appl
30	59	100.0	31	1	US-07-853-408B-83	Sequence 83, Appl
31	59	100.0	31	1	US-08-096-762-83	Sequence 83, Appl
32	59	100.0	31	1	US-08-308-865-83	Sequence 83, Appl
33	59	100.0	31	2	US-09-042-353-280	Sequence 280, App
34	59	100.0	31	2	US-08-758-417A-128	Sequence 128, App
35	59	100.0	31	4	PCT-US92-10983-83	Sequence 83, Appl
36	59	100.0	32	1	US-08-053-131-92	Sequence 92, Appl
37	59	100.0	32	1	US-08-645-641-92	Sequence 92, Appl
38	59	100.0	32	1	US-07-853-408B-92	Sequence 92, Appl
39	59	100.0	32	1	US-08-096-762-92	Sequence 92, Appl
40	59	100.0	32	1	US-08-308-865-92	Sequence 92, Appl
41	59	100.0	32	2	US-09-042-353-289	Sequence 289, App
42	59	100.0	32	2	US-08-758-417A-137	Sequence 137, App
43	59	100.0	32	4	PCT-US92-10983-92	Sequence 92, Appl
44	59	100.0	33	1	US-08-053-131-89	Sequence 89, Appl
45	59	100.0	33	1	US-08-645-641-89	Sequence 89, Appl

ALIGNMENTS

RESULT 1
US-08-471-780C-120
Sequence 120, Application US/08471780C
Patent No. 5759808
GENERAL INFORMATION:
APPLICANT: Casterman, Cecile
APPLICANT: Hamers, Raymond
TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,780C
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958.0008-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-471-780C-120
Query Match 100.0%; Score 59; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11
|||||
Db 1 WGGGTTTVSS 11

RESULT 2
US-08-467-282B-120
; Sequence 120, Application US/08467282B
; Patent No. 5800988
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,282B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Poter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 120:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-467-282B-120

Query Match 100.0%; Score 59; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11
|||||
Db 1 WGGGTTTVSS 11

RESULT 3
US-08-471-282A-120
; Sequence 120, Application US/08471282A
; Patent No. 5840853
; GENERAL INFORMATION:
; APPLICANT: Casterman, Cecile
; APPLICANT: Hamers, Raymond
; TITLE OF INVENTION: Immunoglobulins Devoid of Light Chains
; NUMBER OF SEQUENCES: 130

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,282A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/106,944
; FILING DATE: 17-AUG-1993
; APPLICATION NUMBER: FR 92402326.0
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93401310.3
; FILING DATE: 21-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Poter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 04958.0008-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 120:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-471-282A-120

Query Match 100.0%; Score 59; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11
|||||
Db 1 WGGGTTTVSS 11

RESULT 4
US-08-318-157B-40
; Sequence 40, Application US/08318157B
; Patent No. 5874540
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; APPLICANT: ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CBA HUMANIZED
; TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,157B
; FILING DATE: 05-OCT-1994

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SAKE, Bernhard D.
REGISTRATION NUMBER: 28, 665
REFERENCE/DOCKET NUMBER: 18733/464
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-318-157B-40

Query Match 100.0%; Score 59; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGTTTVSS 11
|||
Db 1 WGGTTTVSS 11

RESULT 5
US-08-466-710C-120
Sequence 120, Application US/08466710C
Patent No. 5874541
GENERAL INFORMATION:
APPLICANT: Casterman, Cecile
TITLE OF INVENTION: Immunoglobulins devoid of light chains
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,710C
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Poter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958, 0008-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-466-710C-120

Query Match 100.0%; Score 59; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGTTTVSS 11
|||
Db 1 WGGTTTVSS 11

RESULT 6
US-08-468-739C-120
Sequence 120, Application US/08468739C
Patent No. 6015695
GENERAL INFORMATION:
APPLICANT: Casterman, Cecile
TITLE OF INVENTION: Immunoglobulins devoid of light chains
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,739C
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,944
FILING DATE: 17-AUG-1993
APPLICATION NUMBER: FR 92402326.0
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93401310.3
FILING DATE: 21-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Poter, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 04958, 0008-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-468-739C-120

Query Match 100.0%; Score 59; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGTTTVSS 11
|||
Db 1 WGGTTTVSS 11

RESULT 7
US-08-646-265A-114
Sequence 114, Application US/0846265A
Patent No. 6214973
GENERAL INFORMATION:

APPLICANT: OHTOMO, Toshiniko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-265A-114

Query Match 100.0%; Score 59; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
|||
Db 1 WGGGTTTVSS 11

RESULT 8
US-08-646-265A-129
Sequence 129, Application US/08646265A
Patent No. 6214973
GENERAL INFORMATION:
APPLICANT: OHTOMO, Toshiniko
APPLICANT: SATO, Koh
APPLICANT: TSUCHIYA, Masayuki
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
TITLE OF INVENTION: MEDULOBLASTOMA CELLS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,265A
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/01763
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-291078
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/184
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 129:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-646-265A-129

Query Match 100.0%; Score 59; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WGGGTTTVSS 11
|||
Db 1 WGGGTTTVSS 11

RESULT 9
US-09-253-794-40
Sequence 40, Application US/09253794
Patent No. 6676924
GENERAL INFORMATION:
APPLICANT: HANSEN, Hans J.
TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODIES
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/253,794
FILING DATE: 22-Feb-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,157
FILING DATE: 05-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: SAYE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 18733/464
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300

/ PRIOR FILING DATE: 1992-08-21
/ PRIOR APPLICATION NUMBER: EPO 93401310.3
/ PRIOR FILING DATE: 1993-05-21
/ NUMBER OF SEQ ID NOS: 130
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 120
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-293-769A-120

Query Match 100.0%; Score 59; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11
Db 1 WGGGTTTVSS 11

RESULT 14
5189147-14
/ Patent No. 5189147
/ APPLICANT: SAITO, HARUO; KRANZ, DAVID M.; EISEN, HERMAN N.;
/ TONEGAWA, SUSUMU
/ TITLE OF INVENTION: METEORODIMERIC T LYMPHOCYTE RECEPTOR
/ ANTI BODY
/ NUMBER OF SEQUENCES: 21
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/271,216
/ FILING DATE: 14-NOV-1988
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 666,988
/ FILING DATE: 31-OCT-1984
/ APPLICATION NUMBER: 620,122
/ FILING DATE: 13-JUN-1984
/ SEQ ID NO: 14
/ LENGTH: 13
5189147-14

Query Match 100.0%; Score 59; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11
Db 3 WGGGTTTVSS 13

RESULT 15
US-08-765-179B-8
/ Sequence 8, Application US/08765179B
/ Patent No. 5854027
/ GENERAL INFORMATION:
/ APPLICANT: STEIBE, Boris
/ APPLICANT: STEINBACHER, Stefan
/ TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY
/ TITLE OF INVENTION: OF ANTIBODIES
/ NUMBER OF SEQUENCES: 28
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
/ STREET: 655 Fifteenth Street N.W. Suite 330
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005-5701
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/765,179B

/ FILING DATE: 14-JAN-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/EP95/02626
/ FILING DATE: 06-JUL-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: DE P 44 25 115.7
/ FILING DATE: 15-JUL-1994
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-765-179B-8

Query Match 100.0%; Score 59; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11
Db 5 WGGGTTTVSS 15

Search completed: December 4, 2005, 04:09:45
Job time : 24.6042 secs

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OM protein - protein search, using sw model

Run on: December 4, 2005, 04:07:28 ; Search time 78.8333 Seconds
(without alignments)
58.302 Million cell updates/sec

Title: US-10-632-706-198

Perfect score: 59

Sequence: 1 WGGGTTVTWSS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA.Main:*

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- 2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep:*
- 5: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep:*
- 6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	11	3	US-09-253-794-40 Sequence 40, Appl
2	59	100.0	11	3	US-09-828-708-78 Sequence 78, Appl
3	59	100.0	11	3	US-09-749-873-114 Sequence 114, Appl
4	59	100.0	11	3	US-09-749-873-129 Sequence 129, Appl
5	59	100.0	11	3	US-09-269-921-137 Sequence 137, Appl
6	59	100.0	11	3	US-09-563-222-157 Sequence 157, Appl
7	59	100.0	11	3	US-09-563-222-165 Sequence 165, Appl
8	59	100.0	11	3	US-09-563-222-181 Sequence 181, Appl
9	59	100.0	11	3	US-09-563-222-197 Sequence 197, Appl
10	59	100.0	11	3	US-09-509-098-117 Sequence 117, Appl
11	59	100.0	11	4	US-10-218-253-137 Sequence 137, Appl
12	59	100.0	11	4	US-10-169-351-40 Sequence 40, Appl
13	59	100.0	11	4	US-10-160-506-40 Sequence 26, Appl
14	59	100.0	11	4	US-10-310-113-26 Sequence 147, Appl
15	59	100.0	11	4	US-10-310-113-147 Sequence 147, Appl
16	59	100.0	11	4	US-10-310-113-148 Sequence 148, Appl
17	59	100.0	11	4	US-10-310-113-149 Sequence 149, Appl
18	59	100.0	11	4	US-10-310-113-150 Sequence 150, Appl
19	59	100.0	11	4	US-10-310-113-151 Sequence 151, Appl
20	59	100.0	11	4	US-10-310-113-152 Sequence 152, Appl
21	59	100.0	11	4	US-10-310-113-153 Sequence 153, Appl
22	59	100.0	11	4	US-10-310-113-154 Sequence 154, Appl
23	59	100.0	11	4	US-10-310-113-155 Sequence 155, Appl
24	59	100.0	11	4	US-10-310-113-156 Sequence 156, Appl
25	59	100.0	11	4	US-10-310-113-157 Sequence 157, Appl
26	59	100.0	11	4	US-10-310-113-158 Sequence 158, Appl
27	59	100.0	11	4	US-10-310-113-159 Sequence 159, Appl

ALIGNMENTS

28	59	100.0	11	4	US-10-412-703A-135	Sequence 135, App
29	59	100.0	11	4	US-10-443-466A-69	Sequence 69, Appl
30	59	100.0	11	4	US-10-443-466A-120	Sequence 120, Appl
31	59	100.0	11	4	US-10-443-379-40	Sequence 40, Appl
32	59	100.0	11	4	US-10-688-015-40	Sequence 195, Appl
33	59	100.0	11	4	US-10-632-706-195	Sequence 198, Appl
34	59	100.0	11	4	US-10-632-706-198	Sequence 201, App
35	59	100.0	11	4	US-10-632-706-201	Sequence 204, App
36	59	100.0	11	4	US-10-632-706-204	Sequence 146, App
37	59	100.0	11	4	US-10-783-950-146	Sequence 166, App
38	59	100.0	11	4	US-10-783-950-169	Sequence 120, App
39	59	100.0	11	4	US-10-160-505-40	Sequence 413, App
40	59	100.0	11	5	US-10-922-068-413	Sequence 78, App
41	59	100.0	11	5	US-10-630-009-78	Sequence 40, Appl
42	59	100.0	11	5	US-10-755-382-40	Sequence 9, Appl
43	59	100.0	11	5	US-10-984-960A-9	Sequence 45, Appl
44	59	100.0	11	5	US-10-984-960A-45	
45	59	100.0	11	5	US-10-984-960A-45	

RESULT 1
US-09-253-794-40
; Sequence 40, Application US/09253794
; Patent No. US20020018750A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hane J.
; ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/253,794
; FILING DATE: 22-Feb-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,157
; FILING DATE: 05-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-253-794-40
Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGTTTVSS 11
| | | | |
Db 1 WGGTTTVSS 11

RESULT 2

US-09-828-708-78
; Sequence 78, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 78
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-78

Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGTTTVSS 11
| | | | |
Db 1 WGGTTTVSS 11

RESULT 3

US-09-749-873-114
; Sequence 114, Application US/09749873
; Publication No. US20030023045A1
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshihiko
; SATO, Koh
; TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/749,873
; FILING DATE: 29-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,265
; FILING DATE: 1996-09-09
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/184
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 114:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 114:

US-09-749-873-114

Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGTTTVSS 11
| | | | |
Db 1 WGGTTTVSS 11

RESULT 4

US-09-749-873-129
; Sequence 129, Application US/09749873
; Publication No. US20030023045A1
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshihiko
; SATO, Koh
; TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/749,873
; FILING DATE: 29-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,265
; FILING DATE: 1996-09-09
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 129:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 129:
US-09-749-873-129

Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11
| | | | |
Db 1 WGGGTTTVSS 11

RESULT 5

US-09-269-921-137
; Sequence 137, Application US/09269921
; Publication No. US20030045691A1
; GENERAL INFORMATION:
; APPLICANT: Ono, Koichiro
; APPLICANT: Ohtomo, Toshiniko
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yoshimura, Yasushi
; APPLICANT: Koishihara, Yasuo
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
; FILE REFERENCE: 35029-20007.00
; CURRENT APPLICATION NUMBER: US/09/269,921
; CURRENT FILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: PCT/JP97/03553
; EARLIER FILING DATE: 1997-10-03
; EARLIER APPLICATION NUMBER: JP 8-264756
; EARLIER FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: JH6
; PUBLICATION INFORMATION:
; AUTHORS: Ravetch, J. et al.
; JOURNAL: CELL
; VOLUME: 27
; PAGES: 583-591
; DATE: 1981
US-09-269-921-137

Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11
| | | | |
Db 1 WGGGTTTVSS 11

RESULT 6

US-09-563-222-157
; Sequence 157, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-157

Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11
| | | | |
Db 1 WGGGTTTVSS 11

RESULT 7

US-09-563-222-165
; Sequence 165, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-165

Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11
| | | | |
Db 1 WGGGTTTVSS 11

RESULT 8

US-09-563-222-181
; Sequence 181, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 181
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-181

Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WGGGTTTVSS 11
| | | | |
Db 1 WGGGTTTVSS 11

RESULT 9

US-09-563-222-197
; Sequence 197, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; TITLE OF INVENTION: EUKARYOTIC CELLS
; FILE REFERENCE: 310098.406

/ CURRENT APPLICATION NUMBER: US/09/563.222
/ CURRENT FILING DATE: 2000-05-02
/ NUMBER OF SEQ ID NOS: 197
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 197
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-563-222-197

Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11
|||
Db 1 WGGGTTTVSS 11

RESULT 10
US-09-509-098-179
/ Sequence 179, Application US/09509098
/ Publication No. US20030103970A1
/ GENERAL INFORMATION:
/ APPLICANT: TSUCHIYA, MASAYUKI
/ TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
/ FILE REFERENCE: 053466/0274
/ CURRENT APPLICATION NUMBER: US/09/509,098
/ PRIOR FILING DATE: 2000-03-22
/ PRIOR APPLICATION NUMBER: PCT/JP98/04469
/ PRIOR FILING DATE: 1998-10-02
/ PRIOR APPLICATION NUMBER: JP 9-271726
/ PRIOR FILING DATE: 1997-10-03
/ NUMBER OF SEQ ID NOS: 203
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 179
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Amino acid
/ OTHER INFORMATION: Sequence of the H chain V region JH6
US-09-509-098-179

Query Match 100.0%; Score 59; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11
|||
Db 1 WGGGTTTVSS 11

RESULT 11
US-10-218-253-137
/ Sequence 137, Application US/10218253
/ Publication No. US20030129185A1
/ GENERAL INFORMATION:
/ APPLICANT: Ono, Koichiro
/ APPLICANT: Ohtomo, Toshiko
/ APPLICANT: Tsuchiya, Masayuki
/ APPLICANT: Yoshimura, Yasushi
/ APPLICANT: Koshihara, Yasuo
/ TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
/ FILE REFERENCE: 35029-20007.00
/ CURRENT APPLICATION NUMBER: US/10/218,253
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US/09/269,921
/ PRIOR FILING DATE: 1999-04-01
/ PRIOR APPLICATION NUMBER: PCT/JP97/03553
/ PRIOR FILING DATE: 1997-10-03
/ PRIOR APPLICATION NUMBER: JP 8-264756
/ PRIOR FILING DATE: 1996-10-04

/ NUMBER OF SEQ ID NOS: 137
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO: 137
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism: JH6
/ PUBLICATION INFORMATION:
/ AUTHORS: Ravetch, J. et al.
/ JOURNAL: CELL
/ VOLUME: 27
/ PAGES: 583-591
/ DATE: 1981
US-10-218-253-137

Query Match 100.0%; Score 59; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11
|||
Db 1 WGGGTTTVSS 11

RESULT 12
US-10-169-351-4
/ Sequence 4, Application US/10169351
/ Publication No. US20030157090A1
/ GENERAL INFORMATION:
/ APPLICANT: BENVENTO, EUGENIO
/ APPLICANT: FRANCONI, ROSELLA
/ APPLICANT: DESIDERIO, ANGIOLA
/ APPLICANT: TAVIADORAKI, PARASKEVI
/ TITLE OF INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANTIBODIES
/ TITLE OF INVENTION: WHICH INCLUDE THEM
/ FILE REFERENCE: 4161-4
/ CURRENT APPLICATION NUMBER: US/10/169,351
/ PRIOR FILING DATE: 2002-10-29
/ PRIOR APPLICATION NUMBER: PCT/IT00/00554
/ PRIOR FILING DATE: 2000-12-29
/ PRIOR APPLICATION NUMBER: IT RM99A000803
/ PRIOR FILING DATE: 1999-12-30
/ NUMBER OF SEQ ID NOS: 118
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 4
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: peptide
US-10-169-351-4

Query Match 100.0%; Score 59; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGGGTTTVSS 11
|||
Db 1 WGGGTTTVSS 11

RESULT 13
US-10-160-506-40
/ Sequence 40, Application US/10160506
/ Publication No. US20030161832A1
/ GENERAL INFORMATION:
/ APPLICANT: Bander, Neil H.
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
/ TITLE OF INVENTION: SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR
/ TITLE OF INVENTION: PROSTATE SPECIFIC MEMBRANE ANTIGEN
/ FILE REFERENCE: 10448-162001

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; CURRENT APPLICATION NUMBER: US/10/160,506
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/324,100
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/362,612
; PRIOR FILING DATE: 2002-03-08
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: deimmunized heavy chain J415-4
US-10-160-506-40

Query Match      100.0%; Score 59; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WGGGTTVTVSS 11
        |||||
Db      1 WGGGTTVTVSS 11

RESULT 14
US-10-310-113-26
; Sequence 26, Application US/10310113
; Publication No. US20030176664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; APPLICANT: NIEVES, ESPERANZA LILIANA
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; TITLE OF INVENTION: THROMBOSES
; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/310,113
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-310-113-26

Query Match      100.0%; Score 59; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WGGGTTVTVSS 11
        |||||
Db      1 WGGGTTVTVSS 11

RESULT 15
US-10-310-113-147
; Sequence 147, Application US/10310113
; Publication No. US20030176664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WONG, HING C.
; APPLICANT: NIEVES, ESPERANZA LILIANA
; APPLICANT: MOSQUERA, LUIS A.
```

```
; TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
; TITLE OF INVENTION: THROMBOSES
; FILE REFERENCE: 58122(71758)
; CURRENT APPLICATION NUMBER: US/10/310,113
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 09/990,586
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/343,306
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/293,854
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 08/814,806
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 147
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: humanized HC-01 FR4 amino acid sequence
US-10-310-113-147
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Query Match      100.0%; Score 59; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WGGGTTVTVSS 11
        |||||
Db      1 WGGGTTVTVSS 11
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Search completed: December 4, 2005, 04:37:44
Job time : 79.8333 secs

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